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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 23:04:22 ; Search time 24231 Seconds
(without alignments)
3379.527 Million cell updates/sec

Title: US-09-367-496C-7
Perfect score: 1690
Sequence: 1 gccgccccctaccagagaccc.....atgaccacatgccgcgcgc 1690

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1690	100.0	1690	6	AB7376 Sequence 7
2	1690	100.0	1690	6	BD070044 Use of UL
3	1689	99.9	1690	9	HSRNU114
4	1686.8	99.8	2699	9	AB006713 Homo sapi
5	1669.2	98.8	2727	11	BV178596 sqm10150
6	1655.8	98.0	1719	6	CQ721242 Sequence
7	1306.8	77.3	2546	10	AB006715 Mus muscu
8	1303.6	77.1	1920	6	AB7374 Sequence 5
9	1303.6	77.1	1920	6	BD070043 Use of UL
10	1303.6	77.1	1920	10	MMULIP4
11	1275	75.4	2489	10	RNU52103
12	1067.2	63.1	2470	5	AF249294
13	1066.8	63.1	1880	5	BX950824
14	1038.6	61.5	2741	5	AF301551
15	995.8	58.9	3884	4	BTU83278
16	980.2	58.0	2947	10	RRT0AD64
17	977	57.8	4450	10	BC062955
18	970.6	57.4	1817	6	AB7370 Sequence 1
19	970.6	57.4	1817	6	BD070041 Use of UL

20	970.6	57.4	1915	10	MMULIP2
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27	963.8	57.0	4614	9	HSN807259
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31	963.8	57.0	5421	6	AX336393
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33	929.6	55.0	2393	5	AF301550
34	929.6	55.0	2423	5	GGU17277
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36	879.8	52.1	2692	10	MMU72875
37	879.6	52.0	2202	5	AF301553
38	878.2	52.0	2296	6	BD070042
39	878.2	52.0	2297	6	AB7372
40	878.2	52.0	2297	10	MMULIP3
41	878.2	52.0	2850	10	BC031738
42	878.2	52.0	2909	10	AB006714
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ALIGNMENTS

RESULT 1
LOCUS AB7376 1690 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 7 from Patent WO9837192.
ACCESSION AB7376
VERSION AB7376.1 GI:6736129
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1690)
AUTHORS Byk, T. and Belin, M.
TITLE USE OF ULIP PROTEINS IN THE DIAGNOSIS AND THERAPY OF CANCER AND
PARANEOPLASTIC NEUROLOGICAL SYNDROMES
JOURNAL Patent: WO 9837192-A 7 27-AUG-1998;
BYK TAMARA (CH); BELIN MARIE FRANCOISE (FR)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.3e-265;
Matches 1690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCGCCCTACCAGAGACCCCGAGGAGGATGTCCTTCCAGGGCAAGAAAGCATCCC 60
Db 1 GCCGCCCTACCAGAGACCCCGAGGAGGATGTCCTTCCAGGGCAAGAAAGCATCCC 60
Qy 61 CCGGATCAGAGTACCGCCTTCTGATCAGAGTGGGAGGATCGTGATGACGACGATC 120
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Db 181 CGTCCCTGGGGGCATCAAGACCAATGACGCCACCGCCTGATGGTCTCTTCTGGTGGCGT 240
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Db 421 GGCCTGTGCGACTACTCTCTGCGACGTGGACATGATCAACCCGATGGCATGAGAGCATCAAGGA 480
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Db 1201 ATCTTCAATTTTATCCCAAGAGGGGAGTGTGGCTGTGGCTGTGAGCTGACTGGT 1260
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Db 1261 CATATGGAAACCCCAAGGACCAAGATCATCTCTGCCAAGACCCCAATCTGAACGTGGA 1320

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Qy 1441 TCGGAAAACATTCGCGGACTTTGTCTACAAGAGATCAAAAGCTCGCAACAGGCTGGCGGA 1500
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Qy 1561 CAAGCCAGGAGTGGCGCTCCGGCCCGCGCTCTCCGCCAGGCAAGATCTCCGTGCCTCC 1620
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Qy 1681 CGCCGAGCGC 1690
Db 1681 CGCCGAGCGC 1690

RESULT 2
BD070044 1690 bp DNA linear PAT 27-AUG-2002
LOCUS Use of ULIP proteins in the diagnosis and therapy of cancer and
DEFINITION paraneoplastic neurological syndromes.

ACCESSION BD070044
VERSION BD070044.1 GI:22615647
KEYWORDS JP 2001512971-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1690)
AUTHORS Aguera, M., Belin, M.F., Honnorat, J., Kolattukudy, P., Quach, T.T.,
Byk, T., Sobel, A. and Aunis, D.
TITLE Use of ULIP proteins in the diagnosis and therapy of cancer and
paraneoplastic neurological syndromes
JOURNAL Patent: JP 2001512971-A 4 28-AUG-2001;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
COMMENT OS Homo sapiens (human)
PN JP 2001512971-A/4
PD 28-AUG-2001
PF 19-FEB-1998 JP 1998536335
PR 19-FEB-1997 FR 97/01961
PI MICHELE AGUERA, MARIE FRANCOISE BELIN, JEROME HONNORAT PI
, PAPPACHAN KOLATTUKUDY,
PI THAN TAM QUACH, TANARA BYK, ANDRE SOBEL, DOMINIQUE AUNIS PC
C12N15/12, C07K14/47, C07K16/18, G01N33/574, C12Q1/68, A61K38/17, PC
A61K48/00,
PC A61K39/395
CC Use of ULIP proteins in the diagnosis and therapy of cancer
and
CC paraneoplastic neurological syndromes
FH Key Location/Qualifiers
FT source 1. .1690
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers

FEATURES
source1. .1690
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ORIGIN

Query Match	100.0%;	Score 1690;	DB 6;	Length 1690;
Best Local	Similarity	100.0%;	Pred. No. 5.3e-265;	
Matches 1690;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	GCGCCCTTACCAGAGACCCCGACGACGAGATGCTCTCCAGGGCAAGAAAGCATCCC	60	
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Qy	61	CCGGATCACAGTAGTACCCGCTTCTGATCAGAGTGGGAGGATCGTGAATGACCAAGTC	120	
Db	61	CCGGATCACAGTAGTACCCGCTTCTGATCAGAGTGGGAGGATCGTGAATGACCAAGTC	120	
Qy	121	CTTTTACGCTGATGTGACGTGGAGATGCGTTGATATAAACTCGAGAAAACTTCAT	180	
Db	121	CTTTTACGCTGATGTGACGTGGAGATGCGTTGATATAAACTCGAGAAAACTTCAT	180	
Qy	181	CGTCCCTGGGGCATCAAGACATTTGACGCCACCGCTGATGTCTCTCTGTGGCGT	240	
Db	181	CGTCCCTGGGGCATCAAGACATTTGACGCCACCGCTGATGTCTCTCTGTGGCGT	240	
Qy	241	TGAGCTCCACAAAGGCTGCAGATGCTCTCTGGGCATGACACCGCTGACGACTTCTG	300	
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Qy	1561	CACGCCAGGAGTGGGCTCCCGGCGCGGCTCTGCCAGGCAAGATCTCCGTGCTGCTCC	1620
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Db	1681	CGCCCGACGC 1690	
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DEFINITION	H.sapiens mRNA for Ulip4 protein.		
ACCESSION	Y10976		
VERSION	Y10976.1	GI:2077995	
KEYWORDS	phosphoprotein.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Byk, T., Ozon, S. and Sobel, A.		
TITLE	The Ulips: a family of proteins associated unc-33 gene product		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1690)		
TITLE	Byk, T.		
JOURNAL	Direct Submission		
COMMENT	Submitted (03-FEB-1997) T. Byk, INSERM U440, 17 rue du Fer a Moulin, F- 75005 Paris, FRANCE		
FEATURES	On May 10, 1997 this sequence version replaced gi:1914866.		
source	Related sequence X87817.		
	Location/Qualifiers		
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ORIGIN

Query Match 99.9%; Score 1689; DB 9; Length 1690;
Best Local Similarity 99.9%; Pred. No. 7.7e-265;
Matches 1689; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GCGCCCTTACAGAGACCCCGAGGACAGGATGTCTTCCAGGGCAAGAAAGCATCCC	60
Db	1	GCGCCCTTACAGAGACCCCGAGGACAGGATGTCTTCCAGGGCAAGAAAGCATCCC	60
Qy	61	CCGGATCAGAGTGACCGCCTTCTGATCAGAGTGGGAGGATCGTGAATCAGACCATC	120
Db	61	CCGGATCAGAGTGACCGCCTTCTGATCAGAGTGGGAGGATCGTGAATCAGACCATC	120
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Db	121	CTTTTACGCTGATGTGCACTGGAAGATGGCTTGATAAAACAAATCGGAGAAACCTCAT	180
Qy	181	CGTCCCTGGGGGATCAAGACCATTTGACGCCACGGCTTGATGGTCTTCTCGTGGCGT	240
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Db	361	CGACAGGGTGTGAGCTGTGCGGCTTACGAGCATGTGCGGAGCGGCGGACAGCGC	420
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Qy	541	CAAGGACCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	600
Db	541	CAAGGACCGGTGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG	600
Qy	601	CTTGGGGGCTTGGCCAGGTGACCGCTGAGAACGGGACATCGTGGAGGAGGACGAA	660
Db	601	CTTGGGGGCTTGGCCAGGTGACCGCTGAGAACGGGACATCGTGGAGGAGGACGAA	660

Qy	661	GCGGTTGCTGGAGCTCGGCATCACTGGCCCCGAGGGGCCAGTGTCTCAGCCACCCGAGGA	720
Db	661	GCGGTTGCTGGAGCTCGGCATCACTGGCCCCGAGGGGCCAGTGTCTCAGCCACCCGAGGA	720
Qy	721	GGTGGAGGCTGAGGCGGTGTACCGAGCTGTCAACATCGCCCAAGCAGGCAAACTGCCGCT	780
Db	721	GGTGGAGGCTGAGGCGGTGTACCGAGCTGTCAACATCGCCCAAGCAGGCAAACTGCCGCT	780
Qy	781	GTAAGTCAACCAAGGTGATGAGCAAGGGGGCGGCGAGCCATCGCTCAGGCCAAGCGCAG	840
Db	781	GTAAGTCAACCAAGGTGATGAGCAAGGGGGCGGCGAGCCATCGCTCAGGCCAAGCGCAG	840
Qy	841	AGGGTGGTCTGTTTGGGAGCCCATCACCGCAGCTGGGCAACCGAGCTTCACTA	900
Db	841	AGGGTGGTCTGTTTGGGAGCCCATCACCGCAGCTGGGCAACCGAGCTTCACTA	900
Qy	901	CTGGAGGAGAACTGGGGCAAGGCTGAGGCTTTCGTCAATCAACCCCTTGTCAACCCAGA	960
Db	901	CTGGAGGAGAACTGGGGCAAGGCTGAGGCTTTCGTCAATCAACCCCTTGTCAACCCAGA	960
Qy	961	CCCCACCGGACAGACCACTCACTGCTTGTCTCCAGCGGGGACCTCCAGGTGACAGG	1020
Db	961	CCCCACCGGACAGACCACTCACTGCTTGTCTCCAGCGGGGACCTCCAGGTGACAGG	1020
Qy	1021	CAGCGCCCACTGCACCTTCACTGCCCAGAGGCTGTGGGCAAGGACAACTTCGCGCT	1080
Db	1021	CAGCGCCCACTGCACCTTCACTGCCCAGAGGCTGTGGGCAAGGACAACTTCGCGCT	1080
Qy	1081	GATCCCGAGGGCACCAACGGCATTTGAGGAGCGCATGTGATGGTCTGGGAGAAATGTGT	1140
Db	1081	GATCCCGAGGGCACCAACGGCATTTGAGGAGCGCATGTGATGGTCTGGGAGAAATGTGT	1140
Qy	1141	GGCTCTGGGAGATGAGGAGGATGAGTTCGTCGCGGTGACCACTACAAATCTGCCAA	1200
Db	1141	GGCTCTGGGAGATGAGGAGGATGAGTTCGTCGCGGTGACCACTACAAATCTGCCAA	1200
Qy	1201	AATCTTCAATTTTACCCAGGAAAGGGGAGTGGCTGTGGGCTCTGACGCTGACCTGGT	1260
Db	1201	AATCTTCAATTTTACCCAGGAAAGGGGAGTGGCTGTGGGCTCTGACGCTGACCTGGT	1260
Qy	1261	CATATGGAAACCCCAAGGCCACCAAGATCATCTCTGCAAGACCAATCTGAACGTGGA	1320
Db	1261	CATATGGAAACCCCAAGGCCACCAAGATCATCTCTGCAAGACCAATCTGAACGTGGA	1320
Qy	1321	GTAACAATCTTGAAGGAGTGGAGTGGCGGGAGCGCTGCGGTGATTAAGTCAGGG	1380
Db	1321	GTAACAATCTTGAAGGAGTGGAGTGGCGGGAGCGCTGCGGTGATTAAGTCAGGG	1380
Qy	1381	CCGAGTGGCGCTGGAGGAGCGGAAAGATGTTTGTACCCCGGGGGCGGCGCTTCGTCCC	1440
Db	1381	CCGAGTGGCGCTGGAGGAGCGGAAAGATGTTTGTACCCCGGGGGCGGCGCTTCGTCCC	1440
Qy	1441	TGGAAGAAATTCGCCGACTTTGTCTAAGAGGATCAAGCTCGCAACAGGTGGCGGA	1500
Db	1441	TGGAAGAAATTCGCCGACTTTGTCTAAGAGGATCAAGCTCGCAACAGGTGGCGGA	1500
Qy	1501	GATCCAGGTGTGCGCGGTGGCTGTATGACGGGGCGGCTCCAGAGGTGATGGTCTGC	1560
Db	1501	GATCCAGGTGTGCGCGGTGGCTGTATGACGGGGCGGCTCCAGAGGTGATGGTCTGC	1560
Qy	1561	CAAGCAGGAGTGGCGCTCGGCGCGCGCTCTGCGCCAGGCAAGATCTCCGTGCTCC	1620
Db	1561	CAAGCAGGAGTGGCGCTCGGCGCGCGCTCTGCGCCAGGCAAGATCTCCGTGCTCC	1620
Qy	1621	TGTGCGCAACCTACATCAGTTCGGGGTTCAGCCTATCTGGGTCTCAGGCTGATGACCAT	1680
Db	1621	TGTGCGCAACCTACATCAGTTCGGGGTTCAGCCTATCTGGGTCTCAGGCTGATGACCAT	1680
Qy	1681	CGCCCGACGC	1690
Db	1681	CGCCCGACGC	1690

RESULT 4	AB006713	2699 bp	mRNA	linear	PRI 22-AUG-1997	238	CTTTTACGCTGATGTGCACGTCGGAAGATGGCTTGATATAAAACAAATCGGAGAAAACCTCAT	297
LOCUS	AB006713	2699 bp	mRNA	linear	PRI 22-AUG-1997	181	CGTCCCTGGGGCGCATCAAGACCATTTGACGCCCAACGGCTGATGGCTCTTCTCTGGTGGCGGT	240
DEFINITION	AB006713	2699 bp	mRNA	linear	PRI 22-AUG-1997	298	CGTCCCTGGGGCGCATCAAGACCATTTGACGCCCAACGGCTGATGGCTCTTCTCTGGTGGCGGT	357
ACCESSION	AB006713	GI:2342485	mRNA	linear	PRI 22-AUG-1997	241	TGACGTCCACACAAAGGCTGCAGATCCCTGTCTCTGGGCAATGACACCGGTGACGATCTTCTG	300
VERSION	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	358	TGACGTCCACACAAAGGCTGCAGATCCCTGTCTCTGGGCAATGACACCGGTGACGATCTTCTG	417
KEYWORDS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	301	TGACGGCCACCAAGGCGGCTGAGAGGAGAACCAACCATGATCTTGGACCAACGCTTCTTCCC	360
SOURCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	418	TGACGGCCACCAAGGCGGCTGAGAGGAGAACCAACCATGATCTTGGACCAACGCTTCTTCCC	477
ORGANISM	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	361	CGACACGGCTGTGAGCTGTCTGGCGGCTTACGAGCAGTGGCGGAGCGGCGGAGCAGCGC	420
REFERENCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	478	CGACACGGGTGTGAGCTGTCTGGCGGCTTACGAGCGGTGGCGGAGCGGCGGAGCAGCGC	537
AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	421	GGCTGTCTGCGACTACTCCCTGACGCTGGAATCAACCGATGGCATGAGAGCATCAAGGA	488
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	538	GGCTGTCTGCGACTACTCCCTGACGCTGGAATCAACCGATGGCATGAGAGCATCAAGGA	597
JOURNAL	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	481	GGAGCTGGAGGCGCTGTCTGGCGGCTTACGAGCAGTGGCGGAGCGGCGGAGCAGCGC	540
MEDLINE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	598	GGAGCTGGAGGCGCTGTCTGGCGGCTTACGAGCAGTGGCGGAGCGGCGGAGCAGCGC	657
PUBMED	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	541	CAAGGACCGGTGCCAGTGCAGCAGCAGCAGATGATGACAGATCTTACAGCATCATCCCGGA	600
REFERENCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	658	CAAGGACCGGTGCCAGTGCAGCAGCAGCAGATGATGACAGATCTTACAGCATCATCCCGGA	717
AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	601	CTTGGGGGCTTTGGGCGCTGACGCTGAGAACGGGAGCATCTGTTGGAGGAGGAGCAGAA	660
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	718	CTTGGGGGCTTTGGGCGCTGACGCTGAGAACGGGAGCATCTGTTGGAGGAGGAGCAGAA	777
JOURNAL	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	661	GGGTTGCTGGAGCTGCGGATCATCTGGGCGGCGAGGCGCATCGTGTCTGACGCAATCCCGGA	720
REFERENCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	778	GGGTTGCTGGAGCTGCGGATCATCTGGGCGGCGAGGCGCATCGTGTCTGACGCAATCCCGGA	837
AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	721	GGTGGAGGCTGAGGCGGCTGTACCGAGCTGTACCGAGCTGTACCATGCCAAGCAGGCAAACTG	780
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	838	GGTGGAGGCTGAGGCGGCTGTACCGAGCTGTACCGAGCTGTACCATGCCAAGCAGGCAAACTG	897
JOURNAL	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	781	GTACGTCCACAAAGGTGATGAGCAAGGGGCGGCGCGAGCCATCGCTCAGGGCAAGCGCAG	840
REFERENCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	898	GTACGTCCACAAAGGTGATGAGCAAGGGGCGGCGCGAGCCATCGCTCAGGGCAAGCGCAG	957
AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	841	AGGGTGTGCTGCTGTTGGGAGCCCATCACGCGCAGCTCTGGGCGACCGACGTTTCACTA	900
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	958	AGGGTGTGCTGCTGTTGGGAGCCCATCACGCGCAGCTCTGGGCGACCGACGTTTCACTA	1017
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AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	961	CCCCACCAAGGCAAGCACTCCTCAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1078	CCCCACCAAGGCAAGCACTCCTCAGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1137
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AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1081	GATCCCGGAGGCGCAACCGGCTATTGAGGAGCGGATGCTGATGCTGCTGCTGCTGCTGCTG	1140
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JOURNAL	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1141	GGCCTCTGGGAGATGGAGCAGAGAT	1200
REFERENCE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1258	GGCCTCTGGGAGATGGAGCAGAGATGAGTTGTCGCGGTGACCAAGTACAAATGCTGCCAA	1317
AUTHORS	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1201	AATCTTTCAATTTTTTACCAAGAGAGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT	1260
TITLE	AB006713.1	GI:2342485	mRNA	linear	PRI 22-AUG-1997	1318	AATCTTTCAATTTTTTACCAAGAGAGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT	1377

QY 1261 CATATGAAACCCCAAGSCCAACAGATCATCTCTGCCAAGACCCACAATCTGAACGTGGA 1320
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 QY 1321 GTACAAACATCTTCAGAGGAGTGAGAGTGCAGGAGAGCCCTGCCGTGGTCAATAGTCAGGG 1380
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 QY 1381 CGAGTGGCGCTGGAGGAGACGGGAAGAGATGTTTGTTCACCCCGGGGCGGCGCTTCGTCC 1440
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 QY 1441 TCGGAAACCAATTCGCCGACTTTCTCTACAAGAGAGATCAAGGCTCGCAACAGGCTGGCGGA 1500
 Db 1558 TCGGAAACCAATTCGCCGACTTTCTCTACAAGAGAGATCAAGGCTCGCAACAGGCTGGCGGA 1617
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 Db 1618 GATCCACGGTGTGCCCGTGGGCTGTATGACGGGCCCGTCCACGAGGTGATGGTGCCTGC 1677
 QY 1561 CAAGCAGGAGTGGCGCTCCGGCCCGCGGCTCTGCCCCAGGCAAGATCTCGTGCCTCC 1620
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 QY 1621 TGTGCGCAACCTACATCAGTCGGGGTTTCAAGCCTATCTGGGTCTCAGGCTGATGACCAAT 1680
 Db 1738 TGTGCGCAACCTACATCAGTCGGGGTTTCAAGCCTATCTGGGTCTCAGGCTGATGACCAAT 1797
 QY 1681 CGCCCCGACGC 1690
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RESULT 5

LOCUS

DEFINITION BVI78596 2727 bp DNA linear STS 10-JUN-2004
 sqm101508 Human DNA (Sequenc) Homo sapiens STS genomic, sequence
 tagged site.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BVI78596.1 GI:48015026
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
 Cantor,C.R. and Braun,A.
 Large-Scale Validation of Single Nucleotide Polymorphisms in Gene

JOURNAL

COMMENT

Genome Res. (2004) In press

Contact: Andreas Braun

Pharmaceuticals division

Sequenom, Inc.

2595 John Hopkins Court, San Diego, CA 92121, USA

Tel: 18582029018

Fax: 18582029020

Email: abraun@sequenom.com

Primer A: No primer sequence submitted

Primer B: No primer sequence submitted

STS size: 2727.

Location/Qualifiers

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/mol_type="genomic DNA"

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<1. .52727

FEATURES

source

ORIGIN

Query Match

Score

Length

DB 11;

2727;

Best Local Similarity 99.5%; Pred. No. 1.2e-261;
 Matches 1682; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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 Db 2558 CCGGATCAGAGTGACCGCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACGATC 2499
 QY 121 CTTTATACGCTGATGTGCACGTGGAGATGGCTTGTATATAAACAATCGGAGAAACCTCAT 180
 Db 2498 CTTTATACGCTGATGTGCACGTGGAGATGGCTTGTATATAAACAATCGGAGATTAACCTCAG 2439
 QY 181 CGTCCCTGGGGGCATCAAGACCAATTGACGCCCAACCGGCTGATGGTCTTCTTGGTGGCGT 240
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 Db 2258 CGACAGGCTGTGAGCTGCTGGCCCTACAGCAGTGGCGGAGCGGCGGAGCAGCGC 2199
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 QY 481 GGAGCTGAGGAGCCCTGGTCAAGGAGAGGAGTGTGAATCTCTTCTGGTCTTTCATGGCATA 540
 Db 2138 GGAGCTGAGGAGCCCTGGTCAAGGAGAGGAGTGTGAATCTCTTCTGGTCTTTCATGGCATA 2079
 QY 541 CAAGGACCGGTGCGAGTGCAGGACGAGCAGATGTACGAGATCTTCAGCATCATCCGGGA 600
 Db 2078 CAAGGACCGGTGCGAGTGCAGGACGAGCAGATGTACGAGATCTTCAGCATCATCCGGGA 2019
 QY 601 CTTGGGGGCTTTGGCCAGGTGCACCTCAGAAACGGGGACATCGTGGAGAGGAGCAGAA 660
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Db	1538	GATCCCGAGGACCAACCGCATTTGAGGAGCGCATGTTCGATGGTCTGGGAGAAATGTGT	1479
Qy	1141	GGCTCTGGGAAGATGACGAGAAATGATTCGTCCGCGGTGACCAATGATCAAAATGCTGCCAA	1200
Db	1478	GGCTCTGGGAAGATGACGAGAAATGATTCGTCCGCGGTGACCAATGATCAAAATGCTGCCAA	1419
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Db	1418	AATCTTCAATTTTACCCAGGAGGCGGAGTGCGTGTGGGCTCTGACGCTGACCTGG	1359
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Db	1358	TCATATGGAACCCCAAGGCCCAACAGATCATCTCTGCCAAGACCCACCAATCTGAACCTGG	1299
Qy	1320	AGTACAAATCTTCGAGGAGTGAGTGCCGGGAGCGCTGCCGTGGTCAATAGTCAGG	1379
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Db	1238	GCCGAGTGCGCTGGAGGACGGGAGAGATTTGTTCACCCGGGGCGGGCGCTTCGTCC	1179
Qy	1440	CTCGGAAAAATCTCCCGGACTTTTGTCTACAGAGGATCAAGCTTCGCAACAGGCTGGCGG	1499
Db	1178	CTCGGAAAAATCTCCCGGACTTTTGTCTACAGAGGATCAAGCTTCGCAACAGGCTGGCGG	1119
Qy	1500	AGATCCACGGTGTCCCGTGGCTGTATACGCGGCCGCTCCACGAGGTGATGGTCTG	1559
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Qy	1560	CCAGGCCAGGAGTGGCGCTCCGCGCCGCGGCTCTGCGGAGGAGATCTCCGCGCTC	1619
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Qy	1620	CTGTGCGCAACCTACATCAGTCGGGGTTTACGCTTATCTGGGTCTTCAGGCTGATGACACA	1679
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Db	938	TGCGCCGACGC 928	
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DEFINITION	Sequence 7176 from Patent WO02068579.		
ACCESSION	CQ721242		
VERSION	CQ721242.1 GI:42282099		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1. Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.		
AUTHORS	Kits, such as nucleic acid arrays, comprising a majority of		
TITLE	humanexons or transcripts, for detecting expression and other uses		
JOURNAL	thereof		
FEATURES	Patent: WO 02068579-A 1716 06-SEP-2002;		
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ORIGIN			
Query Match	98.0%; Score 1655.8; DB 6; Length 1719;		

Best Local Similarity 99.9%; Pred. No. 1.9e-259; Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Qy	92	GGTGGGAGGATCGTGAATGACGACCACTTCTTTTACGCTGATGTCACGCTGGAAGATGGC	151
Db	61	GGTGGGAGGATCGTGAATGACGACCACTTCTTTTACGCTGATGTCACGCTGGAAGATGGC	120
Qy	152	TTGATTAATAAATCGGAGAAACCTTCCTGCTCCCTGGGGGCATCAAGACCATTTGAGGCC	211
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Qy	212	CAGGCGCTGATGTCTTCTCTGTGTGCTTGTAGCTGCACAAAGGCTGCAAGATGCCTGTC	271
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Qy	272	CTGGGCAATGACACCGGCTGACGACTTCTGTTCAGGGCACCAAGGCAGCGCTAGCAGGAGA	331
Db	241	CTGGGCAATGACACCGGCTGACGACTTCTGTTCAGGGCACCAAGGCAGCGCTAGCAGGAGA	300
Qy	332	ACCACCATGATCTTTGGAACCACTTCTCCCGGACACGCGGTGTGAGCTCTGCGCGCTTAC	391
Db	301	ACCACCATGATCTTTGGAACCACTTCTCCCGGACACGCGGTGTGAGCTCTGCGCGCTTAC	360
Qy	392	GAGCAGTGGCGGAGCGGGCGGACAGCGCGCTGTGCGACTACTTCCCTGCACGCTGGAC	451
Db	361	GAGCAGTGGCGGAGCGGGCGGACAGCGCGCTGTGCGACTACTTCCCTGCACGCTGGAC	420
Qy	452	ATCACCCGATGGCATGAGAGCATCAAGAGGAGCTGAGAGCCCTTGGTCAAGAGGAGAGGGT	511
Db	421	ATCACCCGATGGCATGAGAGCATCAAGAGGAGCTGAGAGCCCTTGGTCAAGAGGAGAGGGT	480
Qy	512	GTGAACTCTTCTGTGTCTTATGGGATACAAAGGACCGGTGCGAGCTGACGAGCAG	571
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Qy	692	GAGGGCAATCGTGTCTAGCCACCCCGAGAGGTGGAGGCTGAGCGGTGTACCGAGCTGTC	751
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Qy	872	GCAGCTGGGCAACCGAGGTTTCACTACTTGAGCAAGAACTGGGGCAAGGCTGACGCC	931
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Qy	992	CTGTCCAGCGGGGACCTTCCAGGTGACAGGCGGCGCCACTTGCACCTTACCACTGCCCAG	1051
Db	961	CTGTCCAGCGGGGACCTTCCAGGTGACAGGCGGCGCCACTTGCACCTTACCACTGCCCAG	1020
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Db 1021 AAGGCTGTGGGCAAGCAACATTTTCGGCTGATCCCGAGGGCACCAACGGCATTTGAGGAG 1080
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 VERSION AB006715.1 GI:2342489
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 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (sites) Hamejima, N., Matsuda, K., Sakata, S., Tamaki, N., Sasaki, M. and Nonaka, M.
 TITLE A novel gene family defined by human dihydropyrimidinase and three related proteins with differential tissue distribution
 JOURNAL Gene 180 (1-2), 157-163 (1996)
 MEDLINE 97126821
 PUBMED 8973361
 REFERENCE 2 (sites) Hamejima, N., Kato, Y., Kowaki, M., Wada, Y., Sasaki, M. and Nonaka, M.
 TITLE Novel members of dihydropyrimidinase related protein family
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 2546) Nonaka, M.
 AUTHORS Direct Submission
 TITLE Submitted (19-AUG-1997) Masaru Nonaka, Nagoya City University
 JOURNAL Medical School, Department of Biochemistry; 1 Kawasumi, Mizuho-cho, Mizuho-ku, Nagoya, Aichi 467, Japan

(E-mail: mnonaka@med.nagoya-cu.ac.jp, Tel: 052-853-8145, Fax: 052-842-3955)
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RESULT 8
AB7374
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AB7374
Sequence 5 from Patent WO9837192.
AB7374
AB7374.1 GI:6736128
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1920)
Byk, T. and Belin, M.
USE OF ULIP PROTEINS IN THE DIAGNOSIS AND THERAPY OF CANCER AND
PARANEOPLASTIC NEUROLOGICAL SYNDROMES
Patent: WO 9837192-A 5 27-AUG-1998;
BYK TAMARA (CH); BELIN MARIE FRANCOISE (FR)
Location/Qualifiers
1. 1920
/organism="Mus musculus"
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ORIGIN

Query Match 77.1%; Score 1303.6; DB 6; Length 1920;
Best Local Similarity 86.1%; Pred. No. 3.3e-202;
Matches 1444; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
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BD070043

LOCUS

DEFINITION Use of ULIP proteins in the diagnosis and therapy of cancer and
paraneoplastic neurological syndromes.

ACCESSION

BD070043

VERSION BD070043.1 GI:22615646

KEYWORDS JP 2001512971-A/3.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 1920)

AUTHORS

Aguera,M., Belin,M.F., Honnorat,J., Kolattukudy,P., Quach,T.T.,
Byk,T., Sobel,A. and Aunis,D.

TITLE

Use of ULIP proteins in the diagnosis and therapy of cancer and
paraneoplastic neurological syndromes

JOURNAL

Patent: JP 2001512971-A 3 28-AUG-2001;

COMMENT

INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

OS Mus musculus (mouse)

PN JP 2001512971-A/3

PD 28-AUG-2001

PF 19-FEB-1998 JP 1998536335

PR 19-FEB-1997 FR 97/01961

PI MICHELE AGUERA, MARIE FRANCOISE BELIN, JEROME HONNORAT PI

, PAPPACHAN KOLATTUKUDY,

PI THAN TAM QUACH, TAMARA BYK, ANDRE SOBEL, DOMINIQUE AUNIS PC

C12N15/12, C07K14/47, C07K16/18, G01N33/574, C12Q1/68, A61K38/17, PC

A61K48/00,

PC A61K39/395

CC Use of ULIP proteins in the diagnosis and therapy of cancer

and

CC paraneoplastic neurological syndromes

FH Key Location/Qualifiers

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1..1920

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Best Local Similarity 86.1%; Pred. No. 3.3e-202;

Matches 1444; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy 1632 TACATCAGTCTGGGTTTTCAGCTATCTGCGTCTCAGGCTGATGACCATGATGCCGACG 1689
Db 1702 TGCACCACTGCGGTTTTCAGCTATCTGCGTCTCAGGCTGATGATGATGCCAGACG 1759

RESULT 10
MMULIP4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

MMULIP4
M.musculus mRNA for Ulip4 protein.
Y09079
Y09079.1 GI:1915916
phosphoprotein; Ulip4 gene.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

1. 1920
Byk, T., Ozon, S. and Sobel, A.
The Ulip4: a family of proteins related to the axonal guidance
associated unc-33 gene product
Unpublished
2 (bases 1 to 1920)
Byk, T.
Direct Submission
Submitted (28-OCT-1996) T. Byk, INSERM U440, 17 rue du Per a
Moulin, P- 75005 Paris, FRANCE
Related
Location/Qualifiers
1. 1920
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR outbred strain"
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/db_xref="taxon:10090"
/tissue_type="brain"
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1. 1920
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102. 1820
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gene
CDS

ORIGIN

Query Match 77.1%; Score 1303.6; DB 10; Length 1920;
Best Local Similarity 86.1%; Pred. No. 3.3e-202;
Matches 1444; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy 72 GTGACCGCCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACGAGTCTCTTTTACGCTG 131

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Qy 132 ATGTGACGTTGGAAGATGCTTCAATAAACAATTCGAGAAAACCTCATGTCCTCGGG 191
Db 202 ATCTGTATGTGGAAGACGGTCTGATTAAACAAATTTGAGAAAATCTCATGTCCTCGGG 261
Qy 192 GCATCAAGACCATTTGACGCCCAAGGCTGATGCTCTCTGTTGGGTTGAGTCCACA 251
Db 262 GCATCAAAACCATTCGATGCTCATGAGGCTGATGCTGCTGCTGGGAGTTGACGTTCA 321
Qy 252 CAAGGCTGACAGATGCTCTCTGAGATGACACCGCTGACGACTTCTGTTCAGGACCA 311
Db 322 CCGGCTGACAGATGCTCTGATGAGGATGACCCAGCTGATGATTTCTGTTCAGGACCA 381
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Db 442 TGAGCTGCTGGCAGCTATGAGCAGTTGGCGGACGAGCAGCGCGGCTGCTGGT 501
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Db 502 ACTACTCTTACATGTGGACATTCCTCTGCTGGACGAGACCAAGAGAGAGCTGGAGG 561
Qy 492 CCTGTGTCAAGGAGAGGTTGAACTCTCTCTCTGCTGCTTTCATGAGCATAAAGACCGGT 551
Db 562 CCTAGTCAGGACAAAGGTGTGAATCTCTCTCTGCTTTCATGGCATAAAGACAGGT 621
Qy 552 GCAGTGCAGGACAGCAGATGTACGAGATCTTTCAGCATCATCCGGACCTGGGGCCT 611
Db 622 GCCAGTGTACTGACGCTCAGATATATGAATCTTTCAGCCTCATCCGGACCTGGGAGCTG 681
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Qy 972 CAGACCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
Db 1042 CAGACCACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1101
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Db 1102 GCACCTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1161
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Qy 1572 GTGGCGCTCGGCGCGGCTGCTGCGCAGGCAAGATCTCCGTCCTGCTGCGCAAC 1631
Db 1642 GTGGCACAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1701
Qy 1632 TACATCAGTTCGGGTTTTCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1689
Db 1702 TGACCAAGTTCGGGTTTTCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1759

RESULT 11

RNU52103
LOCUS Rattus norvegicus rcrmp-3 mRNA, partial cds.
DEFINITION Rattus norvegicus rcrmp-3 mRNA, partial cds.
ACCESSION U52103
VERSION U52103.1 GI:1399539

KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 2489)
AUTHORS Wang L.H. and Strittmatter S.M.
TITLE A family of rat CRMP genes is differentially expressed in the nervous system

J. Neurosci. 16 (19), 6197-6207 (1996)
MEDLINE 96424532
PUBMED 8815901

REFERENCE 2 (bases 1 to 2489)
AUTHORS Strittmatter S.M.
TITLE Direct Submission

Submitted (22-MAR-1996) Stephen M. Strittmatter, Neurology, Yale University School of Medicine, 333 Cedar Street, New Haven, CT 06520, USA

FEATURES
source

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ORIGIN

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Qy	116	CAGTCCCTTTAC	GTGATGTG	CA	CGTGGAA	GATGGCTTGATA	AAAAAATAATCGGAGAAAC	175	
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Qy	176	CTCATGCTCTCTG	GGGGGCAT	CA	AAGCAATTA	CGCCCA	CGGCTGATGGTCTTCTCTGGT	235	
Db	122	CTTATCGTCCCT	GGGGGAAT	CA	AAACCAT	CGATGCTCAT	TGGTCTGATGGTACTGGCTGGG	181	
Qy	236	GGCGTTCAGCTG	CCACACA	AAAGCTCGAGATGCTGTCT	GGGCA	TGACACCGGCTGACGAC	295		
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Qy	296	TTCTGTCA	GGGACACA	AGGCGAG	CGCTAG	CA	GAGGAAACCA	CGATGATCTTGACACCA	355
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Qy	416	AGSCGCGCTG	CTCGACTACT	CTCTG	CA	CGTGGACAT	CA	CCCGATGTCATGAGAGCATC	475
Db	362	AGTGACGCTG	CTGTACTCTCTTA	CAGTGGACAT	TT	CCCCGCTGGG	CATGAGAGCAC	421	
Qy	476	AAGGAGGAGCT	GGAGGCCCTGGT	CA	AGGAGAA	GGGTGTGA	ACTCTCTCTGGTCTTTCATG	535	
Db	422	AAAGAGGAGCT	GGAGGCCCTAGT	CA	GGGACA	AAAGGTGTGA	ACTCTCTCTGGTCTTTCATG	481	
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Qy	596	CGGACCT	GGGGGCTTGG	CCCCAGGTGC	ACGCTG	AGAAC	GGGGACATCGTGGAGGAGAG	655	
Db	542	CGGACCT	GGGAGCTGTGTGGCC	CCAGGTGCATGC	AGAA	ACGGGGA	CATCGTGGAGGAGGA	601	
Qy	656	CAGAAG	CGGTTGTG	GAAGCTCGG	GCATCA	CTGGCCCCGAG	GGCCAGTGTCTAGCCAC	715	
Db	602	CAGAAG	CGCCTCTG	CGAGCAGGGGCAT	CA	CTGTCTG	AGGGGCAATGCTCAGGCCACCA	661	
Qy	716	GAGGAGT	GAGGCTG	AGCGGTGTAC	CGAGCTGTCA	CA	TGCCCAAGCGGCAACTGC	775	
Db	662	GAAGAGT	AGAGGCGG	AGCTGTGTAC	AGAGCTGTGA	CCA	TTGCCAAGGAGGCCAACTGC	721	
Qy	776	CCGCTGT	ATCGTCA	CA	CAAGGTGAT	GAGCAAGGGGGCGG	CGCGGATCGCTCAGGCCAAG	835	
Db	722	CCA	CTGTATATCA	CCAAGGTGAT	GAGCAAGGGTGG	CGGCTGATATG	TTGGCCCAAGCCCAAG	781	
Qy	836	CGCAG	AGGGTGTGTGT	TTTGGGAG	GCCATCA	CCGCG	AGCGCTGGGACACGAGCGTTCA	895	
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Db	1509	ATGACGGCGCGGTCCAGGATGTCTCTCAGCACCAAAGCTGTGCCCAACATCGCGCCT	1568
Qy	1586	-----CGCGGCTCTGCGCCAGGCAAGATCTCCGTGCTCTCTGTGGCAACCTACATCAGT	1640
Db	1569	CCAGATCGCGGCTCTGCGCGCAAGATGTGCCCGCGCTGCGCAACTGCACAGT	1628
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DEFINITION			
ACCESSION		EX950824	
VERSION		EX950824.1	GI:42600509
KEYWORDS			
SOURCE		Gallus gallus (chicken)	
ORGANISM		Gallus gallus	
REFERENCE			
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
		1 (bases 1 to 1880)	
		Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E., Croning,M.D.R., Davies,R.M., Prance,M.D., Grafham,D.V., Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R., Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G., Tickle,C. and Wilson,S.A.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickes@ma.umist.ac.uk	
COMMENT		BSRRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA sequencing project.	
		This sequence is from the	
		BSRRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,	
		from a library constructed by Elizabeth Bosch. cDNA was prepared	
		from RNA extracted from whole embryo, normalised, and poly	
		A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector.	
		Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host:	
		Escherichia coli DH10B.	
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Best Local Similarity		77.9%; Pred. No. 1e-163;	
Matches 1300; Conservative		0; Mismatches 362; Indels 6; Gaps 1;	
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Qy	89	AGAGTGGGAGGATCGTGAATGACGACCGTCTCTTTACGCTGATGCGACGTGGAGAT	148
Db	61	AAGGGGGGGAAAATCGTCAACGACGACAGCTGCTTTATCCGCACATTTATGTGGAGAT	120
Qy	149	GGCTTGATAAAACAAATCGGAGAAAACCTCATCGTCTCCCTGGGGGCATCAAGACCATTGAC	208

Db 1201 CGAATCGCGTGGGCTCTGATGACAGACTTGGTCTTGTGGAAACCCAGGGCTACAAAAGTC 1260

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Db 1261 ATCTCGGCAAAAACCCACATTTTGAATGTGGAGTACAACATATTTGAAGGCACCGAGTGT 1320

Qy 1349 CGGGGAGCGCTCGCGTGGTCTAAAGTCAGGGCCGAGTGGCGCTGGAGGACGGGAAGATG 1408

Db 1321 CACGGCGCTCTGCTGTGTCATCAGTCAGGGCAAGAGTCTTTTGAAGACGGGAACCTG 1380

Qy 1409 TTTGTCAACCCCGGGGGCGGCGCTTCTGCTCCCTCGGAACAATTCGCGGACTTTGTCTAC 1468

Db 1381 TTTGTCAACCGAGGCTCGGGGCGCTTCTGTTCCCAAGAAAGAGTTCCGGAATTTGTTAT 1440

Qy 1469 AAGAGATCAAGCTCGCAACAGCTGGCGGAGATCCAGGTGTGCCCGTGGCGCTGTAT 1528

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Qy 1529 GACGGGCGCTCCACAGGTGATGGTGCCTGCCAAGCCAGGAGTGGCGCTCCGGCC--- 1585

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Db 1561 AGGATCGGGCGCTGGCGGCAAGTGGCGCGCTGCCGCAACCTGCACCAAGTCG 1620

Qy 1643 GGGTTAGCTATCTGGGTCTAGGCTGATGACACATCCGCCGAGC 1690

Db 1621 GGGTTAGCTGTGGGCTCGAGGCTGACGACCAAGTTCGCCGGGCGC 1668

RESULT 14

AF301551
LOCUS 2741 bp mRNA linear VRT 06-DEC-2003
DEFINITION Gallus gallus collapsin response mediator protein-3A (CRMP3A) mRNA, complete cds.
ACCESSION AF301551
VERSION AF301551.1 GI:33340026
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2741)
Yuuasa-Kawada, J., Suzuki, R., Kano, F., Ohkawara, T., Murata, M. and Noda, M.
Axonal morphogenesis controlled by antagonistic roles of two CRMP subtypes in microtubule organization
Eur. J. Neurosci. 17 (11), 2329-2343 (2003)
JOURNAL MEDLINE
PUBMED 22699123
12814366
REFERENCE 2 (bases 1 to 2741)
Yuuasa-Kawada, J. and Noda, M.
Direct Submission
Submitted (01-SEP-2000) Molecular Neurobiology, National Institute for Basic Biology, 38 Nishigonaka, Myodaiji-cho, Okazaki, Aichi 444-8585, Japan
JOURNAL
FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 61.5%; Score 1038.6; DB 5; Length 2741;
Best Local Similarity 77.9%; Pred. No. 3.6e-159;
Matches 1267; Conservative 0; Mismatches 354; Indels 6; Gaps 1;

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Db 333 GAGCGAGCAGCTGCTGATCAAGGGGGGAAATCGTCAAGCAGCAGCAGTCTGTTTATGC 392

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Db 393 CGACATTTATGTGGAAGATGGGTGATAAAAACAGATTGGAGAGAACCTGGCTGTCCCGAG 452

Qy 190 GGGCATCAAGACCATTTGACGCCACGCGCTGATGGTCTTCTGCTGGGCGGTGACCTCCA 249

Db 453 CGGGGTGAGGACGGTGGATGCCCTATGGGCGAGCTGGTGGTGGCGGCGGATCATGATGCA 512

Qy 250 CACAAGCTGCGAGATGCTGCTCTGGGCGATGACACCGGCTGACGAGCTTCTGTCAAGGGCAC 309

Db 513 CACGGGCTGCAGATGGCTGTGATGGGATGGCTCTGCTGATGACTTCTACCAAGGCAC 572

Qy 310 CAAAGCAGCGCTAGCAGGAGAACCAACATGATCTTTGGACCAGCTTCTCCCGACAGGG 369

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Qy 370 TGTGAGCTGCTGGCGGCGCTACGAGCAGTGGCGGGAGCGGGGACAGCGCGCGCTGCTG 429

Db 633 GACGAGCTGCTGGCTGCTTACGAGCAGTGGCGGCGAGCGTGTGACAGCGAGGCGCTGCTG 692

Qy 430 CGACTACTCCCTGCGACGTGGACATCACCCGATGGCATGAGAGCATCAAGAGAGAGCTGGA 489

Db 693 CGACTACGCGTGCACATCGACATCCCCGCTGGCACGAGAGCGCTCGCGGAGGAGCTGGA 752

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Qy 670 GAGCTCGGCAATCATCTGGCGCCGAGGGCCACGTGCTGACGCCACCCGAGAGAGTGGAGGC 729

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Db 1053 CAAATAATGAGCAAAAGTGCACGATGTGGTAGTCTCAAGCAAAAGAGAAAGGCACGTGT 1112

Qy 850 CGTGTGTTGGGAGCCCATCATCCGCCAGCTTGGGCAACGAGCGTTTCACTACTTGGAGCAA 909

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Qy	740	TACCGAGCTGTCAACCATCGCCAGCAGGCAAACTGGCCGCTGTACGTCAACCAAGTGTATG	799
Db	885	AACCGTTCCATCAACCATCGCCCAACAGCAACACTGGCTCTCTGTACATCAACCAAGTGTATG	944
Qy	800	AGCAAGGGGGCGGCGCAGCGCATCGCTCAGGCCAAGCGCAGAGGGGTGTCTGTCTTGGG	859
Db	945	AGCAAGAGCGGAGCGGGAAGTTATCGCCAGGCGCGGAAAGGGAACCGTGTGTGTACGGC	1004
Qy	860	GAGCCCATCACCGCAGCCTGGGACACGACGGTTTCACTACTGGAGCAAGAACTGGGCC	919
Db	1005	GAGCCCATCACCGCAGCTTGGGACCGACGGCTCTCACTACTGGAGCAAGAACTGGGCC	1064
Qy	920	AAGCTCGAGCTTCGTCACTACACCCCTGTGTAAACCCAGACCCCAACCGGCGAGCCAC	979
Db	1065	AAGCTCTGCTTTTGTTCACCTCCCGCCCTGAGCCCGCAACCACTCCAGACTTT	1124
Qy	980	CTCACCTGCTTGTCTACGCGGGGACCTCCAGGTGACAGCGAGCGCCACTGCACCTTC	1039
Db	1125	CTGAATCTCTTGTCTGTGTGGAGATCTCCAGGTGACCGGAGTGTCTACTGTACTCTTC	1184
Qy	1040	ACCACTGCCAGAAAGGCTGTGGGCAAGGACAACTTCGCGCTGTATCCCGGAGGCAACCAAC	1099
Db	1185	AACAGGCCCAGAGGCGGTGGAAAGACAACTTCACTCTGATCTCTGAGGCAACCAAC	1244
Qy	1100	GGCAATTGAGGAGCGCATGTGTGATGGTCTGGGAGAAATGTGTGGCTCTGGGAAGATGGAC	1159
Db	1245	GGCACGGAGGAGCGATGTCTGTCTCATCTGGGATTAAGGCTGTGGTCACTGGGAAGATGGAC	1304
Qy	1160	GAGAACTAGTTCTGTCGGGTGACACAGTACAAATGCTGCCAAATCTTCAATTTTACCCA	1219
Db	1305	GAGAACAGTTTGTGGCCGCGTACAGACCAATGCTGCCAAAGTCTTCAACCTGTGTACCCC	1364
Qy	1220	AGGAAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGTGTCTATGGAACCCCAAGGCC	1279
Db	1365	CGGAAGGGCGCATTTGCTGTGGGTCTGATGCTGACTTGGTCACTCTGGGACCCCGACAGC	1424
Qy	1280	ACCAAGATCATCTCTGCGAAGACCCACAATCTGAACCTGGAGTACAACTCTTCGAGGGA	1339
Db	1425	GTGAAGACCATCTCTGCGAAGACCCACAACAGCTCTCTTGAGTACAACTCTTGAAGGC	1484
Qy	1340	GTGAGTGTCCGGGAGCGCTGCGGTGGTCAATAGTCAGGGCCGAGGTGGCGCTGGAGGAC	1399
Db	1485	ATGAGTGTCCGAGGCTCCCCACTGGTGGTCACTAGCCAGGGGAAGATTGTCTGGAGGAT	1544
Qy	1400	GGGAAGATGTTTGTCACCCCGGGGCGGGCGCTTCGTCTCCCTCGGAAAAATTCCTCCGAGC	1459
Db	1545	GGTACCTCTCATGTCAACGAAGGCTCTGGGCGCTACATCCCCCGGAAGCCCTTCCCTGAC	1604
Qy	1460	TTTGTCTCAAGAGGATCAAAAGCTCGCAACAGGCTGGCGGAGATCCACGTTGTGCCCGGT	1519
Db	1605	TTCTGTTTCAAGCGTATCAAGGCAAGGACAGGCTGGCGGAGCTGAGAGGGGTTCCCGGT	1664
Qy	1520	GGGCTGTATGACGGGCGGTCCACGAGGTGATGTGTGCTGTCCCAAGCCAGGGAGTGGCGCT	1579
Db	1665	GGTCTGTACGACGCACTGTGTGGAGGTGTCTGTGACACCAAGACGGTCACTCCCGGCC	1724
Qy	1580	CCGCGCCGCGGCTCTGCGCAGGCAAGATCTCCGTGCTCTCTGTGCGCAACCTACATCAG	1639
Db	1725	TCCTGGGTAAAGCTCTCCGGCCAGACGACGAGCGCCCACTGTCTCCGGAACCTGCACAG	1784
Qy	1640	TCGGGGTTACGCTTATCTGGGTCTCAGGCTGATACCACTATCGCCCCGACGC	1690

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

September 23, 2005, 23:03:07 ; Search time 3115 Seconds
(without alignments)

3211.673 Million cell updates/sec

Title:

US-09-367-496C-7

Perfect score:

1690

Sequence:

1 gccgccctaccagagacc.....atgaccacatgcccgagcgc 1690

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched:

4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
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12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1690	100.0	1690	6	ABK91191 Human cdn
2	1688.4	99.9	1690	2	AAV60818 Human par
3	1688.4	99.9	2741	12	ADQ23110 Human sof
4	1686.8	99.8	2699	12	ADQ18667 Human sof
5	1318.4	78.0	2352	9	AD57506 Human enz
6	1303.6	77.1	1920	2	AAV60817 Mouse ULI
7	1087.2	63.1	2470	12	ADK70708 Collapsin
8	1038.6	61.5	2741	12	ADK70695 Chicken C
9	980.2	58.0	2947	12	ADJ84229 Malayan b
10	970.6	57.4	1817	2	AAV60815 Mouse ULI
11	965.4	57.1	1829	6	ABK91188 Human cdn
12	963.8	57.0	4459	9	ACF25352 Human di
13	963.8	57.0	4459	10	ADC66333 Human di
14	963.8	57.0	4459	13	ADR98995 Dihydroxy
15	963.8	57.0	5421	6	ABL68565 Kidney ca
16	963.8	57.0	5421	6	ABL68565 Lung can
17	963.8	57.0	5421	10	ADC66325 Human col
18	963.8	57.0	5421	10	ADH28910 Human chr
19	963.8	57.0	5421	13	ADR52683 Drug ther
20	963.8	57.0	5421	13	ADT93859 Non-small

21	929.6	55.0	2393	12	ADK70706	Adk70706 Collapsin
22	902.4	53.4	2488	12	ADK70693	Adk70693 Chicken C
23	879.6	52.0	2202	12	ADK70710	Adk70710 Collapsin
24	878.2	52.0	2297	2	AAV60816	AAV60816 Mouse ULI
25	876.8	51.9	2869	10	ADJ56545	Adj56545 Murine cd
26	876.8	51.9	2928	11	ADN95177	Adn95177 Human BEC
27	876.8	51.9	2928	13	ACN38089	Acn38089 Tumour-as
28	875.2	51.8	2797	13	ADR07554	Adr07554 Full leng
29	875.2	51.8	2842	6	ABK91190	Abk91190 Human cdn
30	875.2	51.8	2842	6	ABK39752	Abk39752 cDNA enco
31	875.2	51.8	2842	8	ACA12081	Acad12081 Human lun
32	875.2	51.8	2842	8	ACA03267	Acad03267 Lung can
33	875.2	51.8	2842	10	ADH47319	Adh47319 Human lun
34	875.2	51.8	2842	13	ADJ21238	Adj21238 Human lun
35	873.4	51.7	1719	8	ACC48980	Acc48980 Human col
36	868.6	51.4	2813	10	ADB59112	Adb59112 Toxicity-
37	850.6	50.3	5046	6	ABL61765	AbL61765 Colon ade
38	850.6	50.3	5047	5	AAH81784	Aah81784 Human dif
39	850.6	50.3	5047	6	ABL65185	AbL65185 Lung can
40	850.6	50.3	5047	11	ADP65042	Adp65042 Human di
41	850.6	50.3	5047	11	ADP65567	Adp65567 Human mRN
42	850.6	50.3	5047	12	ADN03726	Adn03726 Antipeori
43	850.6	50.3	5200	10	ADJ56540	Adj56540 Chicken c
44	850.6	50.3	5250	4	AAL26651	Aal26651 Human bre
45	850.6	50.3	5578	11	ACN88655	Acn88655 Breast ca

ALIGNMENTS

RESULT 1

ABK91191

ID ABK91191 standard; cDNA; 1690 BP.

XX ABK91191;

AC ABK91191;

DT 05-NOV-2002 (first entry)

XX Human cDNA encoding partial Ulip4/CRMP3 protein.

DE Human; ss; gene; Ulip4; CRMP3 collapsin response mediator protein;

XX Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;

KW paraneoplastic neurodegenerative disease; PND; myelination;

KW demyelination; remyelination; myelin disorder; multiple sclerosis;

KW autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;

KW human T lymphocyte virus 1.

XX Homo sapiens.

OS Key

XX CDS

XX Location/Qualifiers

32..1689

/*tag= a

FT /partial

FT /product= "Amino acids 1-553 of Ulip4/CRMP3"

FT /note= "This sequence is stated to encode Ulip4/CRMP3

protein appearing as ABG32231, but only encodes amino

acids 1-553"

FT /transl_except= (pos:197..199,aa:His)

US2002119944-A1.

29-AUG-2002.

09-NOV-2001; 2001US-00986632.

09-NOV-2000; 2000US-0246751P.

(AGUE/) AGUERA M.

(BELI/) BELIN M.

(CHAR/) CHARRIER E.

(HONO/) HONORAT J.

(RICA/) RICARD D.

(ROGE/) ROGEMOND V.

XX Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;
XX MPI; 2002-627172/67.
XX Prevention or treatment of myelin disorders, such as multiple sclerosis,
PT by administering an agent selected from a Ulp1/CRMP protein, a nucleic
PT acid coding for the protein, or an antibody directed against protein.
XX
XX Disclosure; Page 25-26; 44pp; English.
XX The invention relates to a new method for prevention or treatment of
CC myelin disorders, comprises administering to a patient an effective
CC amount of an agent selected from a Ulp1 (Unc-33-like protein)/CRMP
CC (collapsin response mediator protein) protein, a nucleic acid coding for
CC Ulp1/CRMP, an antisense sequence capable of specifically hybridizing with
CC the nucleic acid, an antibody directed against Ulp1/CRMP, or an aptamer
CC capable of binding Ulp1/CRMP, and a pharmacologically acceptable carrier.
CC Also included are methods of diagnosing a myelin disorder in a subject,
CC identifying agents useful for the prevention or treatment of myelin
CC disorders, using the Ulp1/CRMP proteins/nucleic acids, agents capable of
CC modulating the function or expression of the proteins (increasing or
CC decreasing), and a method for identifying an endogenous agent as a
CC therapeutic target for the prevention or the treatment of myelin
CC disorders. The agents are useful for preventing or treating a myelin
CC disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus
CC 1) associated myelopathy and neurodegenerative diseases, Alzheimer's
CC disease, paraneoplastic neurodegenerative diseases (PND), autoimmune
CC neurodegenerative disorder. Ulp1/CRMP proteins are involved in
CC the processes of myelination, demyelination and remyelination. Antibodies
CC to a Ulp1/CRMP protein are useful for diagnosing a myelin disorder. The
CC present sequence encodes a partial Ulp1/CRMP3 protein
XX
SQ Sequence 1690 BP; 360 A; 505 C; 539 G; 286 T; 0 U; 0 Other;
Query Match 100.0%; Score 1690; DB 6; Length 1690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCGCCCTACAGAGACCCAGGAGCAGGATGTCTTCCAGGGCAAGAAAGCATCC 60
DB 1 GCCGCCCTACAGAGACCCAGGAGCAGGATGTCTTCCAGGGCAAGAAAGCATCC 60
QY 61 CCGGATCAGAGTGACCGCTTCTGATCAGAGTGGGAGGATCGTGAATCAGCACCATC 120
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QY 121 CTTTACGCTGATGTCACGTGGAAGATGGCTTGAATAAAACAAATCGAGAAACCTCAT 180
DB 121 CTTTACGCTGATGTCACGTGGAAGATGGCTTGAATAAAACAAATCGAGAAACCTCAT 180
QY 181 CGTCCCTGGGGCATCAAGACCAATTGACGCCACCGGCTGTATGCTCTTCTGGTGGCGT 240
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QY 301 TCAGGGCACCAGGACGCTAGCAGAGGAAACCAACATGATCTTGGACACGCTTCTCC 360
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QY 361 CGACAGGGGTGAGCTGCTGGCGCTACGAGCATGCGGAGCGGGCGGACAGCGC 420
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QY 421 GGCTGCTGCGACTACTCTCTGCGATGACATCACCAGTGGCATGAGAGCATCAAGGA 480
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DB 481 CGAGCTGGAGGCCCTGGTCAAGGAGAGGGGTGTGAATCTCTTCTGGTCTTCAATGGCATA 540
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DB 601 CTTGGGGGCTTTGGGCCAGGTGCAGCTCAGAAACGGGGACATCTGTGGAGAGGAGCAGAA 660
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DB 661 GCGGTGCTGGAGCTCGGCATCACTGGCCCCGAGGGCCACGCTGCTCAGCCACCCCGAGGA 720
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DB 721 GGTGGAGGCTGAGGCGGTGTACCGAGCTGTACCATTCGCAAGCAGGCAAACTGCCCGCT 780
QY 781 GTACGTCAACAAAGGTGATGAGCAAGGGGCGCGGCGGCGCATCGCTCAGGCCAAGCGCAG 840
DB 781 GTACGTCAACAAAGGTGATGAGCAAGGGGCGCGGCGGCGCATCGCTCAGGCCAAGCGCAG 840
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DB 841 AGGGGTGCTGCTGTTTGGGGAGCCCATCACCGCAGCCTGGGCAACGAGGTTCACTA 900
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DB 1501 GATCCACGCTGTGCCCGGTGTATGACGGGCGCTCCAGAGGTGATGTGTGCTGCTGC 1560
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Db 1621 TGTGCGCAACTACATCAGTCGGGGTTACGCTATCTGGGTCTCAGCTGATGACCAAT 1680
Qy 1681 GCGCCGACGC 1690
Db 1681 GCGCCGACGC 1690
RESULT 2
AAV60818
ID AAV60818 standard; cDNA; 1690 BP.
AC AAV60818;
XX 08-DEC-1998 (first entry)
XX Human partial ULIP-4 coding sequence.
XX Human; Unc-33-like phospho-protein; ULIP; rat; neoplasm; tumourigenesis;
KW neurodegenerative disorder; diagnosis; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 32..1690
FT /*tag= a
FT /product= "partial ULIP-4"
FT /notes= "Unc-33-like phosphoprotein 4"
FT /transl_except= (pos: 197..199, aa: Xaa)
FT /note= "Xaa = unknown; codon at this position is given in
FT sequence as a stop codon and may alter the reading frame"
XX PR2759701-A1.
XX 21-AUG-1998.
XX 19-FEB-1997; 97PR-00001961.
XX 19-FEB-1997; 97PR-00001961.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX Aguera M, Belin MF, Homnorat J, Kolattukudy P, Quach TT, Byk T;
PI Sobel A;
XX WPI; 1998-449610/39.
DR P-PSDB; AAW68489.
XX Mouse and human ULIP poly:peptide(s) - useful in detection of para-
neoplastic neurological syndromes.
PS Claim 3; Fig 12; 90pp; French.
XX This sequence represents a partial human Unc-33-like phospho-protein
CC (ULIP)-4 coding sequence. The sequence was isolated based on similarity
CC to the rat ULIP sequence. Proteins of the ULIP family or their
CC corresponding nucleic acids can be used in compositions for treating
CC neurodegenerative disorders and neoplasms, especially for para-neoplastic
CC neurological syndromes and/or for the early diagnosis of tumourigenesis
XX
SQ Sequence 1690 BP; 359 A; 505 C; 539 G; 287 T; 0 U; 0 Other;
Query Match 99.98; Score 1688.4; DB 2; Length 1690;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCGCCCTACAGAGACCCCGAGGAGGATGCTCCAGGGCAAGAAAGCATCCC 60
Db 1 GCGCCCTACAGAGACCCCGAGGAGGATGCTCCAGGGCAAGAAAGCATCCC 60
Qy 61 CCGGATCACGAGTGACCGCCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCGATC 120

Db 61 CCGGATCACGAGTGACCGCCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCGATC 120
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Db 1141 GGCCTCTGGAGATGAGAGAAATGAGTTGCTGGCGGTGACCAATGATGCTGCCAA 1200
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Db 1381 CCGAGTGGCGCTGAGGACGGGAGATGTTTGTACCCCGGGGGCGGCGCTTCCTCC 1440
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Db 1681 CGCCCGAGCGC 1690

RESULT 3
ID ADQ23110
XX ADQ23110 standard; DNA; 2741 BP.
AC ADQ23110;
XX
XX
DT 26-AUG-2004 (first entry)
XX
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 5930.
DB soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
XX ds.
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX

PS Example 2; SEQ ID NO 5930; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 2741 BP; 558 A; 871 C; 839 G; 473 T; 0 U; 0 Other;
Query Match 99.9%; Score 1688.4; DB 12; Length 2741;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCGCGCCCTACAGAGACCCCGAGGAGCAGGATGCTCTCCAGGGCAAGAAAGCATCC 60
Db 118 GCGCGCCCTACAGAGACCCCGAGGAGCAGGATGCTCTCCAGGGCAAGAAAGCATCC 177
Qy 61 CCGGATCAGAGTGACCGGCTTCTGATCAGAGTGGGAGGATCGTGAATGACGACCATC 120
Db 178 CCGGATCAGAGTGACCGGCTTCTGATCAGAGTGGGAGGATCGTGAATGACGACCATC 237
Qy 121 CTTTACGCTGATGTCAGTGGAGATGGCTTGTATATAAACAATCGAGAGAACTCAT 180
Db 238 CTTTACGCTGATGTCAGTGGAGATGGCTTGTATATAAACAATCGAGAGAACTCAT 297
Qy 181 CGTCCCTGGGGCATCAAGACCAATTGACGCCCAAGCCCTGATGGTCTTCTGGTGGCGT 240
Db 298 CGTCCCTGGGGCATCAAGACCAATTGACGCCCAAGCCCTGATGGTCTTCTGGTGGCGT 357
Qy 241 TGACGTCCACACAGGCTGAGATGGCTGTCTGGGATGACACCGGCTGACGACTTCG 300
Db 358 TGACGTCCACACAGGCTGAGATGGCTGTCTGGGATGACACCGGCTGACGACTTCG 417
Qy 301 TCAGGGCACACAGGCGCTAGCAGGAGAACCAACCATGATCTTGGACCAAGCTTCCC 360
Db 418 TCAGGGCACACAGGCGCTAGCAGGAGAACCAACCATGATCTTGGACCAAGCTTCCC 477
Qy 361 CGACAGGCTGTAGGCTGCTGGCGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGC 420
Db 478 CGACAGGCTGTAGGCTGCTGGCGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGC 537
Qy 421 GGCCTGCTGGGACTACTCCCTGACGTGACATCACCCGATGCGATGAGAGCATCAAGGA 480
Db 538 GGCCTGCTGGGACTACTCCCTGACGTGACATCACCCGATGCGATGAGAGCATCAAGGA 597
Qy 481 GAGCTGAGGAGGCTCTGCTCAAGGAGAGGCTGTGAATCTCTCTCTCTTCAATGGCATA 540
Db 598 GAGCTGAGGAGGCTCTGCTCAAGGAGAGGCTGTGAATCTCTCTCTCTTCAATGGCATA 657
Qy 541 CAAGGACCGGCTGACGTGACGACAGCCAGATGTACAGAGATCTTCAGCATCATCCGGGA 600
Db 658 CAAGGACCGGCTGACGTGACGACAGCCAGATGTACAGAGATCTTCAGCATCATCCGGGA 717
Qy 601 CTTGGGGGCTTGGCCAGGTCACGCTGAGAACCGGGGATCTGTGAGGAGGAGCAGAA 660
Db 718 CTTGGGGGCTTGGCCAGGTCACGCTGAGAACCGGGGATCTGTGAGGAGGAGCAGAA 777
Qy 661 GCGGTTGCTGGAGCTCGGATCACTGGCCCGAGGCGCACGCTCTCAGCCACCCGAGGA 720
Db 778 GCGGTTGCTGGAGCTCGGATCACTGGCCCGAGGCGCACGCTCTCAGCCACCCGAGGA 837
Qy 721 GGTGAGGCTGAGGCGGCTGTACCGAGCTGTACCATCGCAAGAGAGGCAAACTGCCCGCT 780
Db 838 GGTGAGGCTGAGGCGGCTGTACCGAGCTGTACCATCGCAAGAGAGGCAAACTGCCCGCT 897

CC with decreased expression or overexpression of functional ENZM. The
CC disorders include immune disorders (anemia, allergy or asthma),
CC infectious disorders (viral, fungal, parasitic or protozoal infection),
CC immune deficiencies (acquired immune deficiency syndrome; AIDS),
CC metabolic disorders (Addison's disease, diabetes or goitre), reproductive
CC disorders (infertility or impotence), cardiovascular disorders
CC (atherosclerosis or myocardial infarction), eye disorders and cell
CC proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
CC present sequence is human ENZM cDNA
XX
SQ Sequence 2352 BP; 471 A; 768 C; 711 G; 402 T; 0 U; 0 Other;

Query Match 78.0%; Score 1318.4; DB 9; Length 2352;
Best Local Similarity 89.3%; Pred. No. 1.4e-260;
Matches 1509; Conservative 0; Mismatches 1; Indels 180; Gaps 1;

QY 1 GCGCCCTTACCAGAGACCCAGGACGAGTCTCTCCAGGGCAAGAAAGCATCCC 60
DB 63 GCGCCCTTACCAGAGACCCAGGACGAGTCTCTCCAGGGCAAGAAAGCATCCC 122
QY 61 CCGGATCAGAGTGACCGCCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCAAGTC 120
DB 123 CCGGATCAGAGTGACCGCCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCAAGTC 182
QY 121 CTTTACGCTGATGTGACGCTGGAAGATGGCTTGATATAAAACAAATCGGAGAAACCTCAT 180
DB 183 CTTTACGCTGATGTGACGCTGGAAGATGGCTTGATATAAAACAAATCGGAGAAACCTCAT 242
QY 181 CGTCCCTGGGGGATCAAGACCAATTGACGCGCCAGCGCTGATGCTCTCTGGTGGCGT 240
DB 243 CGTCCCTGGGGGATCAAGACCAATTGACGCGCCAGCGCTGATGCTCTCTGGTGGCGT 302
QY 241 TGAAGCTCACAAAGGCTGCAGATGCTCTGGGATGACACCGGCTGACGACTTCTG 300
DB 303 TGAAGCTCACAAAGGCTGCAGATGCTCTGGGATGACACCGGCTGACGACTTCTG 362
QY 301 TCAGGGACCAAGGACGCTAGCAGAGGAAACCAATGATTTGGAACCAAGCTTTCCC 360
DB 363 TCAGGGACCAAGGACGCTAGCAGAGGAAACCAATGATTTGGAACCAAGCTTTCCC 422
QY 361 CGACAGGCTGAGCTGCTGGCGCTACGAGCAGTGGGGAGCGGGGCGGACGCG 420
DB 423 CGACAGGCTGAGCTGCTGGCGCTACGAGCAGTGGGGAGCGGGGCGGACGCG 482
QY 421 GGCTGTGCGACTACTCTCTGCACTGAGCATCAACCGATGGCATGAGAGCATCAAGGA 480
DB 483 GGCTGTGCGACTACTCTCTGCACTGAGCATCAACCGATGGCATGAGAGCATCAAGGA 542
QY 481 GGAAGTGGAGGCTGTGCTGAAGAGAAAGGTGTGAATCTCTTCTGCTTTCAATGGAATA 540
DB 543 GGAAGTGGAGGCTGTGCTGAAGAGAAAGGTGTGAATCTCTTCTGCTTTCAATGGAATA 602
QY 541 CAAGGACCGGTGCGAGTGACGACGACGATGTACGATCTTCAAGCATCTCCGGGA 600
DB 603 CAAGGACCGGTGCGAGTGACGACGACGATGTACGATCTTCAAGCATCTCCGGGA 662
QY 601 CTTGGGGGCTTGGCCCAAGGTGACGCTGAGAAACGGGGACATCGTGGAGGAGGAGGAA 660
DB 663 CTTGGGGGCTTGGCCCAAGGTGACGCTGAGAAACGGGGACATCGTGGAGGAGGAGGAA 722
QY 661 GCGGTTGCTGGAGCTCGGCATCACTGCGCCCGAGGGGACAGTGTCTAGCCACCCGAGGA 720
DB 723 GCGGTTGCTGGAGCTCGGCATCACTGCGCCCGAGGGGACAGTGTCTAGCCACCCGAGGA 782
QY 721 GGTGGAGGCTGAGCGGTGTACCGAGCTGTCAACATCGCCAGGCAAACTGCCCGCT 780
DB 783 GGTGGAGGCTGAGCGGTGTACCGAGCTGTCAACATCGCCAGGCAAACTGCCCGCT 842
QY 781 GTACGTCACCAAGGTGATGAGCAAGGGGGCGGCGCATCGCTCAGGCCAAGCGCAG 840
DB 843 GTACGTCACCAAGGTGATGAGCAAGGGGGCGGCGCATCGCTCAGGCCAAGCGCAG 902
QY 841 AGGGGTGGTGTGTTGGGGAGGCCCATCACCGCAGCGCTGGGCAACCGGTTCACTA 900

DB 903 AGGGGTGGTGTGTTTGGGGAGCCCATCACCGCAGCCTGGGACCCGAGCTTTCACACTA 962
QY 901 CTGGAGCAAGAACTGGGGCCAAAGGCTGACGCTTTCGTGCATCAACCCCTCTGCAACCCAGA 960
DB 963 CTGGAGCAAGAACTGGGGCCAAAGGCTGACGCTTTCGTGCATCAACCCCTCTGCAACCCAGA 1022
QY 961 CCCACCAACGCGAGACCACTCACTGCTTGTGTCTCAGCGGGGACCTCCAGGTGACAGG 1020
DB 1023 CCCACCAACGCGAGACCACTCACTGCTTGTGTCTCAGCGGGGACCTCCAGGTGACAGG 1082
QY 1021 CAGGCGCCATGCACTTACCACTGCGCCAGAGAGGCTGTGGGCAAGCAAACTTCGCGCT 1080
DB 1083 CAGGCGCCATGCACTTACCACTGCGCCAGAGAGGCTGTGGGCAAGCAAACTTCGCGCT 1142
QY 1081 GATCCCGGAGGGCACCAACGGCATTCAGGAGCGCATGTCTGATGTCTCTGGGAGAAATGTGT 1140
DB 1143 GATCCCGGAGGGCACCAACGGCATTCAGGAGCGCATGTCTGATGTCTCTGGGAGAAATGTGT 1202
QY 1141 GGCTCTCTGGAGAGTGGACGAGAAATGAGTTGCTGCGGGTGACCAAGTACAAATGTGCCAA 1200
DB 1203 GGCTCTCTGGAGAGTGGACGAGAAATGAGTTGCTGCGGGTGACCAAGTACAAATGTGCCAA 1262
QY 1201 AATCTTCAATTTTACCCAAAGGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT 1260
DB 1263 AATCTTCAATTTTACCCAAAGGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT 1322
QY 1261 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCGCAAGACCAACANTCT 1320
DB 1323 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCGCAAGACCAACANTCT 1373
QY 1321 GTACAACATCTTTCAGGGAGTGGAGTGGCCGGGAGCGCTGCGGTGTGTCTAATGTCAGGG 1380
DB 1374 ----- 1373
QY 1381 CCGAGTGGCGCTGGAGGACGGGAGAGATGTTTGTCA CCGCGGGGGCGGCGCTTTCGTCCTC 1440
DB 1374 ----- 1373
QY 1441 TCGGAAAAATTCCTCCGAGCTTTGTCTCAAGAGGATCAAGCTCGCAACAGGCTGGCGGA 1500
DB 1374 -----GCTGGCGGA 1382
QY 1501 GATTCACGCTGTGCTCCCGTGGGCTGTATGACGCGGCCCTGTCACAGAGTGTATGTGCTGC 1560
DB 1383 GATTCACGCTGTGCTCCCGTGGGCTGTATGACGCGGCCCTGTCACAGAGTGTATGTGCTGC 1442
QY 1561 CAAGCAGGAGGTGGGCTCTCCGCGCCGCGGTCTGCGCCAGGCAAGATCTTCGTCCTCC 1620
DB 1443 CAAGCAGGAGGTGGGCTCTCCGCGCCGCGGTCTGCGCCAGGCAAGATCTTCGTCCTCC 1502
QY 1621 TGTGCGCAACCTACATCAGTTCGGGGTTTACGCTTATCTGGGTCTCAGGCTGATGACCAT 1680
DB 1503 TGTGCGCAACCTACATCAGTTCGGGGTTTACGCTTATCTGGGTCTCAGGCTGATGACCAT 1562
QY 1681 CGCCCGACGC 1690
DB 1563 CGCCCGACGC 1572

RESULT 6

AAV60817

ID AAV60817 standard; cDNA; 1920 BP.

XX AAV60817;

AC AAV60817;

XX 08-DEC-1998 (first entry)

DT Mouse ULIP-4 coding sequence.

XX Mouse; Unc-33-like phospho-protein; ULIP; rat; neoplasm; tumorigenesis;

XX neurodegenerative disorder; diagnosis; ss.

XX

OS Mus musculus.

XX Key Location/Qualifiers

FT CDS 102..1820

FT /*tag= a

FT /product= "ULIP-4"

FT /note= "Unc-33-like phosphoprotein 4"

XX

PN FR2759701-A1.

XX

XX 21-AUG-1998.

XX

XX 19-FEB-1997; 97PR-00001961.

XX

XX 19-FEB-1997; 97PR-00001961.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Aguera M, Belin MF, Honnorat J, Kolattukudy P, Quach TT, Byk T; Sobel A;

XX

DR WPI; 1998-449610/39.

XX P-PSDB; AAW68488.

XX

XX Mouse and human ULIP poly:peptide(s) - useful in detection of para-neoplastic neurological syndromes.

XX

XX Claim 3; Fig 11; 90pp; French.

XX

XX This sequence represents the mouse Unc-33-like phospho-protein (ULIP)-4 coding sequence. The sequence was isolated based on similarity to the rat ULIP sequence. Proteins of the ULIP family or their corresponding nucleic acids can be used in compositions for treating neurodegenerative disorders and neoplasms, especially for para-neoplastic neurological syndromes and/or for the early diagnosis of tumorigenesis

XX

SQ Sequence 1920 BP; 440 A; 524 C; 562 G; 394 T; 0 U; 0 Other;

Query Match 77.1%; Score 1303.6; DB 2; Length 1920;

Best Local Similarity 86.1%; Pred. No. 1.5e-257;

Matches 1444; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 12 CAGAGACCCACGAGGATGCTCTCCAGGCGAAGAAAGCATCCCGGATACGA 71

DB 82 CAGCCCGCGTGTATCAGGATGCTCTCCAGGCGAAGAAAGCATCTCCCGATACGA 141

QY 72 GTACCGCCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACCACTCTTTACGCTG 131

DB 142 GCGACCGCCTTCTCATCAAGGTGGGAAGATTGTGAACGATGACCACTCTTCATGCTG 201

QY 132 ATGTGACGTTGGAAGATGGCTTGATATAAACAATTCGAGAGAAACCTCATGCTCCGCGG 191

DB 202 ATCTGTATGTGGAAGACGGTCTGATTAACAATAATTTGGAGAAATCTCATGCTCCGCGG 261

QY 192 GCATCAAGACCATGAGCCGACCGCTGATGTCCTTCTGCTGGGTTGAGCTCCACA 251

DB 262 GCATCAAAACCATGATGCTCATGCTGATGCTGCTGCTGGGAGATTGAGCTTCACA 321

QY 252 CAAGGCTGAGATGCCCTGTCTCGGCAATGACACCGCTGACGACTTCTGTGAGGACCA 311

DB 322 CCGGCTGCAGATGCCCTGTGATGGCAATGACCCAGCTGATGATTTCTGTGAGGACCA 381

QY 312 AGGAGCGCTAGCAGAGGAAACCAACATGATCTTTGACCAAGCTTCCCGGACACGGGTG 371

DB 382 AGCGGCTCTAGCAGGCGGACCAACATGATATTTGGACCATGTTGTTCTGACGCTGGTG 441

QY 372 TGAGCTGCTGGCGCTTACAGCAGTGGCGGAGCGGGCGGACAGCGCGCTGCTGCG 431

DB 442 TGAGCTGCTGGCAGCTTATAGCAGTGGCGGAGCGGACAGCAGCGCGCTGCTGCTG 501

QY 432 ACTACTCCCTGACGTTGACATCAACCGATGGCATGAGAGCATCAAGGAGGAGCTGGAGG 491

DB 502 ACTACTCCCTTACATGTGGACATTTCTCTGCTGGCACGAGACCAACAAAGAGAGCTGGAGG 561

QY 492 CCTGCTCAAGGAGAGGGTGTGAACCTCTTCTGCTCTCATGGCATACAGGACGGCT 551

DB 562 CCTAGTCAAGGACAAAGGTGTGAACCTCTTCTGCTCTCATGGCATACAGGACGGT 621

QY 552 GCCAGTGCAGGCACAGCCAGATGTACGAGATCTTTCAGCATCATCCGGGACCTTGGGGGCT 611

DB 622 GCCAGTGTACTGACGGTCAAGATATATGAATCTTTCAGCCTCATCCGGGACCTTGGGAGCTG 681

QY 612 TGGCCCAAGGTGCA CGCTGAGAA CGGGGACAT CGTGGAGAGGAGCAGAAAGCGGTTCTG 671

DB 682 TGGCCCAAGGTGCA CGCGAGAAAT TGGGACAT CGTGGAGAGGAAACAGAAAGCGCTGCTG 741

QY 672 AGCTCGGCATCACTGGCCCCGAGGGCCACGTGCTAGCCACCCCGAGGAGGTGGAGGCTG 731

DB 742 AGCAAGGCATCACTGGTCTGAGGGCCATGTGCTAGCCACCCAGAAAGGAGGTAGAGGCGG 801

QY 732 AGGCGGTGTACCGAGCTGTCAACATCGCCAAGCAGGCAAACTGCCCGCTGTAGCTACCA 791

DB 802 AGGCTGTGTACAGAGCATCAACATTTGCCAAGCAGGCGCAACTGCCCACTATAGCTACCA 861

QY 792 AGGTGATGAGCAAGGGGGCGGCGACGCATCGCTCAGGCCAAGCCGAGAGGGGTGGTGC 851

DB 862 AGGTGATGAGCAAGGGGTGCGAGCTGACATGCTTGCCAAGCCAAAGCGCAGGGGGTGGTGC 921

QY 852 TGTTTGGGAGCCCATCAGCGCCAGCTGGGCGACCGAGCGTTACACTACTTGGAGCAAGA 911

DB 922 TCTTTGGGAAACCTATCACTGCCAGCTGGGCACTGATGGCTCACACTACTTGGAGCAAGA 981

QY 912 ACTGGGCCAAGGCTGAGCGCTTTCGTCAATCAATACCCCTCTCAACCCAGACCCACCAACCG 971

DB 982 ACTGGGCCAAGGCTGAGCGCTTTCGTCACTTACCCCTTATCAACCCGAGACCTTACTG 1041

QY 972 CAGACCACTCACTCTGCTGTGTCAGCGGGGACCTTCCAGGTGACAGGAGCGGCCACT 1031

DB 1042 CAGACCACTCACTCTGCTGTGTCAGTGGGGACCTTCCAGGTGACAGGAGTGGCCACT 1101

QY 1032 GCACCTTCACTGCGCCAGAGGCTGTGGGCAAGGACAACTTCGCGCTGATCCCGGAGG 1091

DB 1102 GCACCTTCACTGCGCCAGAGGCTGTGGGCAAGGACAACTTCACTGATCCCGGAGG 1161

QY 1092 GCACCAACGGCATTTAGAGGAGCGCATGTCATGCTGCGGAGAAATGTGTGGCTCTGGGA 1151

DB 1162 TAGTCAACGGTATAGAGAGCGCATGTCGTGCTGCGGAGAAATGTGTGGCTTCAAGGA 1221

QY 1152 AGATGGAACGAGAAATGATGCTGCGCGTGAACAAGTACAAATGCTGCCAAATCTTCAATT 1211

DB 1222 AAATGGAACGAGAAATGATGCTGCGCGTGAACAAGTACAAATGCTGCCAAATCTTCAATT 1281

QY 1212 TTTTACCAAGGAGGGCGAGTGGCTGCTGCGGCTCTGACGCTGACCTGCTCATATGGAAC 1271

DB 1282 TTTTACCAAGGAGGGCGAGTGGCTGCTGCGGCTCTGATGCTGACCTGCTGATCTGGAAC 1341

QY 1272 CCAAGGCCACCAAGATCATCTCTGCCAAGACCCACAATCTGAACTGGAGTACAACTCT 1331

DB 1342 CCAAGGCCACCAAGTCACTCTCTGCCAAGACCAATCACTGATGTAGAGTACAACTCT 1401

QY 1332 TCAGGAGTGGAGTCCCGGGAGCGCTGCGGTGTGTCATAAGTCAAGGCGCGAGTGGCGC 1391

DB 1402 TTGAAGAGTGGAGTCCCGAGGAGTGCCCAAGTGGTGTCTAAGTCAAGGCGCAGAGTGGTC 1461

QY 1392 TGGAGGACGGGAGATGTTTGTACCCCGGGGGCGGCGCTTCGTCCTCGGAAACAT 1451

DB 1462 TGGAGGACGGGAAACCTGCTGTCTCAGGGGGCTGGCGCTTCATTTCCCGGAGACGT 1521

QY 1452 TCCCGGACTTTTGTCTACAAGAGGATCAAAAGCTCGCAACAGGCTGGCGGAGATCCAGGTG 1511

DB 1522 TCCCGGACTTTTGTCTATAGAGGATAAAGCTCGCAACAGGCTAGCAGAGATCCAGGTG 1581

QY 1512 TGCCCCGTGGGCTGTATGACGGGCCCGCTCCACAGGCTGATGGTGCCTGCCAAGCCAGGGA 1571

DB 1582 TGCTTCGAGGCTGTACGACGGGCCGTGTGCTGAAGTGTGTTTACCTGCCAAGCCAGGA 1641

QY 1572 GTGGCGCTCCGGCCCGCGCGTCTGCGCCAGGCAAGATCTCGTGCCCTCTCTGTGCGCAACC 1631
Db 1642 GTGGCACACAGGCCCGTGCATCTCTGTTCAGGCAAGATCTCAGTGCACCCGCTGCGCAACC 1701
QY 1632 TACATCAGTCGGGCTTCAGGCTATCTGCTGCTCAGGCTGATGACCATCGCCGAGC 1689
Db 1702 TGCACCAAGTCGGGTTTCAGGCTATCTGCTCTCAGGCTGAGATCACAATTGCCAGAGC 1759

RESULT 7
ADK70708
ID ADK70708 standard; DNA; 2470 BP.
XX
AC ADK70708;
XX
DT 06-MAY-2004 (first entry)
XX
DE Collapsin response mediator protein (CRMP) 3B DNA SeqID.
XX
KW gene; de; signal control molecule; collapsin response mediator protein;
KW CRMP; nerve growth cone; axial future edge; neural-network formation;
KW cell polarity; neurogenesis.
XX
OS Unidentified.
XX
PN JP200400094-A.
XX
PD 08-JAN-2004.
XX
PP 31-MAY-2002; 2002JP-00160853.
XX
PR 31-MAY-2002; 2002JP-00160853.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2004-085208/09.
DR P-PSDB; ADK70709.
XX
XX Novel N-terminal variant polypeptide of signal control molecule collapsin
PT response mediator protein of nerve growth cone, useful for neural-network
PT formation.
XX
PS Disclosure; Fig 18; 94pp; Japanese.
XX
CC This invention relates to a novel variant of an intracellular signal
CC control molecule identified as the collapsin response mediator protein
CC (CRMP) that works within the steering mechanism of the nerve growth cone
CC in an axial future edge part. Specifically, it refers to an N-terminal
CC variant that exhibits a deletion, substitution or addition of an amino
CC acid in CRMP, as well as the appropriate monoclonal antibody. The present
CC invention describes the CRMP variant as useful for neural-network
CC formation and for the establishment of cell polarity during growth.
CC Furthermore, it can be efficiently used during the neurogenesis process.
CC This polynucleotide sequence is DNA encoding a CRMP isoform of the
CC invention.
XX
SQ Sequence 2470 BP; 533 A; 685 C; 757 G; 495 T; 0 U; 0 Other;

Query Match 53.1%; Score 1067.2; DB 12; Length 2470;
Best Local Similarity 77.9%; Pred. No. 4.4e-209;
Matches 1301; Conservative 0; Mismatches 363; Indels 6; Gaps 1;

QY 27 GCAGGATGTCCTTCCAGGCGCAAGAAAGCATCCCGGATCAGAGTGACCGCTTCTGA 86
Db 9 GGAAGATGTCGAACCCCGGCAAGAGGAGCGCCCGCGGCACGAGGACGCTGCTGA 69
QY 87 TCAGAGTGGGAGGATGCTGAATGACGACCAAGTCCTTTTACGCTGATGTGCAAGTGAAG 146
Db 69 TCAAGGGGGGAAATCGTCAACGACGACCAAGTCAGTCTTTTATGCCGACATTTATGTGAAG 128
QY 147 ATGGCTTGATAAAACAAATCGGAGAAACCTCATCTGCTCCCTGGGGGATCAAGACCATG 206
Db 129 ATGGGTGTGATAAACAGATTGGAGAGAACTTGCTGTGTTCCAGCGGGGTGAGGACGGTGG 188

QY 207 ACGCCCAACGCGCTGATGGTCTTCTCTGGTGGCGTTGACGTCCACACAAAGGCTGCAGATGC 266
Db 189 ATGCTTACGGGCAAGCTGGTGGTGGCGGCGCATCGATGTGCACACGCGCTGCAGATGG 248
QY 267 CTGTCTCTGGGCATGACACCGGCTGACGACTTCTGTGTAAGGSCACCAAGGCAAGCTAGCAG 326
Db 249 CTGTGATGGGGATGGGCTCTGCTGATGACTTTTACCAAGGCAAGAGGCGCGCTGCGG 308
QY 327 GAGGAACCAACCATGATCTTGGACACAGCTCTTCCCGACACAGGCTGTGAGCTGTGCGG 386
Db 309 GAGGAACCAACCATGATGATGGAACACAGTGTGCTGCCGAGGCTGGGACGAGCTGTGCTG 368
QY 387 CTTACGAGCAGTGGCGGAGCGGCGGACAGCGCGCTGTCTGCGACTACTCTCTGCAAG 446
Db 369 CTTACGAGCAGTGGCGGAGCGGCTGTGACAGCAGGCGCTGTCTGCGACTACTCTGCGCA 428
QY 447 TGGACATCACCCGATGGCATGAGAGCATCAAGAGGAGCTGGAGGCGCTGTGTAAGAGA 506
Db 429 TCGACATCCCGCTGGCATGAGAGCTTGGCGGAGGAGCTGGAGGCGCTGTGTAAGAGA 488
QY 507 AGGCTGTGAATCTCTTCTGGTCTTCATGSCATACAAGGACCGGTGCCAGTGCAGGACA 566
Db 489 AGGCTGTGAATCTCTTCTGGTCTTATGCGCTTACAAGGACAGCTGCTGAGTGCAGCG 548
QY 567 GCCAGATGTACGAGATCTTTCAGCATCATCCGGGACCTTGGGGCGCTTGGGCCAGGTGCACG 626
Db 549 CCAGATGTATGAATATTTCTGCATTTATTCGAGACCTTGGGGCGCATAGCCCAAGTGCACG 608
QY 627 CTGAGAAACGGGAGCATCTGTGGAGGAGGAGCAGAAAGCGGTGTGTGGAGCTCGGCATCACTG 686
Db 609 CTGAAAACGGGAGCATCATCGAGGAGGAGCAGAAAGAGGCTGTGTGACATTTGGGATCACTG 668
QY 687 GCGCCGAGGGCGACGTGCTCAGCCACCGCGAGGAGGTGGAGGCTGAGGCGGTGTACCGAG 746
Db 669 GGCAGAGGGGGCACGTCTGAGCCGCTCTGAGAGGTTGAAGCAGAGGCGGTGTACCGTG 728
QY 747 CTGTCAACCATCGCAAGCAGGCAAACTTGGCCGCTGTACGCTCACCAAGGTGATGAGCAAGG 806
Db 729 CAATTACATAGCAAAACAGCAACTTGCCTTGTACGTCACCAAAATATAGCDAAA 788
QY 807 GGGCGCGGACGCGCATCTGCTCAGGCGCAAGCGCAGAGGGTGTGTGTTTGGGAGGCCA 866
Db 789 GTGCAGCAGATGTGGTAGCTCAAGCAAGAGAAAGGCACTGTGTGTACGGGAGGCCA 848
QY 867 TCACGCCAGCCTGGGACCGAGCGTTACACTTCTGAGCAGAGACTTGGGCCAAGGCTG 926
Db 849 TCACTCCAGCCTGGGTGCTGACGGCTCGACCTACTTGGAGCAAGAACTTGGGCCAAGGCTG 908
QY 927 CAGCCTTCTGTCACATCACCCCTGTCAACCCAGAGACCCACCGGAGACCACTCACTC 986
Db 909 CAGCCTTCTGTCACCTCACCCCGCTCAGCCCGGACCCACCGGAGAGCGCTCTCTCT 968
QY 987 GCTTGTCTCAGCGGGGACCTTCCAGGTGACAGGCGGCGCCACTGCACCTTCAACACTG 1046
Db 969 CCTGTGTCTGTGGGAGCCTGACGCTGCGAGGCTGTCTACTGCACTTCACTACCG 1028
QY 1047 CCCAGAGGCTGTGGGCAAGGACACTTCCGCTGATCCCGGAGGSCACCAAGCGCATTG 1106
Db 1029 CCCAGAGGCGCGTGGGGAGAGGACACTTCCACCTCATCCCGAGGGGAGCAATGGGATCG 1088
QY 1107 AGGAGCGCATGTGATGGTCTGGGAGAAATGTGTGGCTCTGGGAGAGATGGAGAGATG 1166
Db 1089 AGAGCGGATGGGCATTAATCTGGAGAGAGTGTGTGTCTCAGGAGAGATGATGAGAGC 1148
QY 1167 AGTTCTCGCGTGACAGTACAAATGCTGCCAAATATCTTCAATTTTACCCAAAGAGG 1226
Db 1149 ATTCTGTGGCGGTGACGACACTTAATGCTGCCAAATCTTTAACTGCTACCCAGAGAG 1208
QY 1227 GGGGAGTGTGTGGGCTGTGAGCGCTGACCTGTGATATGGAACCCAGGCGCACCAAGAGA 1286
Db 1209 GSGCAATCGCGGTGGGCTCTGATGACAGACTTGTGCTTGTGGAAACCCAGGCGGTACAAAAG 1268

QY 1030 CTGCACCTTCAACCACTGCCCCAGAGGCTGTGTGGCAAGGACAACTTCGCGCTGTATCCCGCA 1089
Db 1293 CTGCACGTTCACTACCGCCCAAGAGGCGTGTGGGAAGGACAACTTCACCCCTCATCCCGCA 1352
QY 1090 GGGCACCAACGGCAATGAGAGCGCATCTCATGGTCTTGGGAGAAATGTGTGGCTCTGG 1149
Db 1353 GGGGACGAATGGCATCGAGAGCGGATGGCCATTAATCTGGGAGAAATGTGTGGCTCTCAGG 1412
QY 1150 GAAGATGACGAGAAATGAGTTCTGCGGCTGACCAAGTACAAATCTGCGCAAAATCTTCAA 1209
Db 1413 GAAGATGGATGAGAAACGATTTCTGTGGCGGTGACCAAGTACAAATCTTCAA 1472
QY 1210 TTTTACCCAGGAAGGGCGAGTGTGTGGGCTCTGACGCTGACTGTGTATATGAA 1269
Db 1473 CTGTACCCAGGAAGGGCGAATCGCGTGTGGGCTCTGATGACACTTGTCTTGTGGAA 1532
QY 1270 CCCCAGGCCACCAAGATCATCTCTGCCAGACCCACAACTCTGAACGTGGAGTACACAT 1329
Db 1533 CCCCAGGGCTACAAAGTCTCTCGGCAAAACCAATTTGAATGTGGAGTACAAAT 1592
QY 1330 CTTCCAGGGAGTGGAGTGC CGGGAGCGCTCTGCCGTGTCTATAGTCAAGGCCCGAGTGGC 1389
Db 1593 ATTTGAAGGCACGAGTGTCAAGCGCTCTCTGTGTGTCTATCATGTCAGGGGCAAGTGT 1652
QY 1390 GCTGAGGACGAGGAAGATTTGTTCACCGCGGGCGGCGCTTCTGCTCCCTCGGAAAC 1449
Db 1653 TCTTGAGGACGGGAACCTGTTTGTACCGAGGGCTCGGGCGCTTCTGCTCCAGAAAGAC 1712
QY 1450 ATTCCCGGACTTCTCTACAGAGGATCAAGCTCGCAACAGCGCTGGCGGAGTCCACGG 1509
Db 1713 GTTCCCGGATTTGTATTAAAGAAATTAAGCGGAGGAACAGGCTGGCGGAGTGCACGG 1772
QY 1510 TGTCCCGCTGGGCTGTATGACGGGCGCGTCCACGAGTGTATGTGCTGCTGCAAGCCAGG 1569
Db 1773 TGTCCCAAGGGGCTGTATGAGCGCGGCTCCAGATGTGCTCTCAGACCAAGTGT 1832
QY 1570 GAGTGGGCTCCGCGC-----CGCGCTCTGCCAGGCAAGATCTCCGTGCTCTCTGT 1623
Db 1833 GCCCACCATCGCGGCTCCAGGATCGGCGCTGCGCGGCAAGTGTGCGCGCGTCCGCT 1892
QY 1624 GCGCAACTACATCAGTGGGGTTTCAAGCTATCTGGGCTCTCAGGCTGATGACCACTCGC 1683
Db 1893 GCGCAACTGACAGTGGGGTTTCAAGCTATCTGGGCTCTCAGGCTGATGACCACTCGC 1952
QY 1684 CCGACGC 1690
Db 1953 CCGGCGC 1959

RESULT 9

ADJ84229
ID ADJ84229 standard; DNA; 2947 BP.
XX AC ADJ84229;
XX XX
XX 06-MAY-2004 (first entry)
XX XX
XX Malayan black rat CRMP-2 DNA which is a target for antisense therapy.
XX XX
XX antimicrobial; antinflammatory; cytostatic; infection; inflammation;
XX KW tumour formation; antisense therapy; Malayan black rat; CRMP-2;
XX KW collapse response mediator protein 2; ds; target; gene.
XX XX
XX Rattus rattus.
XX XX
XX WO2004003134-A2.
XX XX
XX 08-JAN-2004.
XX XX
XX 12-JUN-2003; 2003WO-US018481.
XX XX
XX 26-JUN-2002; 2002US-0392020P.
XX XX

(ISIS-) ISIS PHARM INC.

Monia BP, Freier SM, Manoharan M, Gaarde WA;

WPI; 2004-083026/08.

P-PSDB; ADJ84279.

Decreasing levels of a preselected cellular mRNA in a cell, useful for treating or preventing a disease associated with a preselected cellular mRNA, comprises binding to the mRNA an antisense compound targeted to a splice site on the mRNA.

Example 19; SEQ ID NO 48; 174pp; English.

The invention relates to a novel method for decreasing levels of a preselected cellular mRNA in a cell or tissue comprising binding to the preselected cellular mRNA an antisense compound which is specifically hybridisable with a splice site on the mRNA and which is not a substrate for RNase H when bound to the RNA. The method of the invention has an antimicrobial, antinflammatory and cytostatic applications and may be useful for decreasing levels of a preselected cellular mRNA in a cell or tissue and thus for treating or preventing a disease or condition associated with a preselected cellular mRNA or with a preselected target cellular protein, particularly infection, inflammation or tumour formation. The current sequence is that of the Malayan black rat CRMP-2 (collapse response mediator protein 2) DNA of the invention which is a target for antisense therapy.

SQ Sequence 2947 BP; 666 A; 765 C; 769 G; 747 T; 0 U; 0 Other;

Query Match 58.0%; Score 980.2; DB 12; Length 2947;

Best Local Similarity 74.1%; Pred. No. 3.1e-191;

Matches 1240; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

QY 18 CCCCCAGGAGCAGGATGCTCTCCAGGCAAGAAAGCATCCCCCGATCAGAGTGACC 77
Db 164 CGCCCCCGGAGAGATGCTTATCAGGGGAAGAAAAATATCCACGCATCAGAGCGATC 223
QY 78 GCCTCTGTGATCAGAGTGGGAGGATCGTGAATGACGACCACTCTTTTACGCTGATGTC 137
Db 224 GTCTTCTGATCAAGGTGGCAAGTTGTGATGATGACCACTCTTCTATGACAGCATAT 283
QY 138 ACOTGGAAGATGGCTTTGATATAAAACAAATCGGAGAAAACCTCATCGTCCCTGGGGCATCA 197
Db 284 ACATGGAAGATGGTTGATCAAGCAATAGGAGAAAACCTGATTTGTCAGGAGGGGTGA 343
QY 198 AGACCAATTGACGCCCAAGGCTGATGCTCTCTGCTGGCTTGAGCTGCACACAAGGC 257
Db 344 AGACCAATGAAAGCCCACTCCAGAAATGGTATCCCTGGAGGAATGACGTCACACTCGCT 403
QY 258 TGCAGATGCTGTCTCTGGGCGATGACACCGGCTGACGACTTCTGTCAGGGCACCAGGCAG 317
Db 404 TCCGATGCCAGACCGAGGAATGACATCAGTGTATGATGATCTTCTCCAGGAGAACAGGCAG 463
QY 318 CGCTAGCAGAGGAACCAACCATGATCTTGGACCAACGCTCTTCCCGGACACCGGGTGTGAGCC 377
Db 464 CCCTGCCCGAGGAACCAACCATGATCATCGACCATGTTGCTCTGAGCCCGGACAGGC 523
QY 378 TGTCTGGGCTCTACGAGCAGTGGCGGAGCGGCGGACAGCGCGGCTGTGCTGACTACT 437
Db 524 TATTGGCAGCCTTTGATCAGTGGAGGGAGTGGGCGGACAGCAAGTCTCTGCTGACTATT 583
QY 438 CCTGTCAGCTGGACATCACCCGATGCGATGAGAGCATCAAGGAGGAGCTGGAGGCCCTGG 497
Db 584 CGCTGCACGTGGACATCAGGAGTGGCAACAGGGCAATCCAGGAGGAGATGGAAGCTCTGG 643
QY 498 TCAAGGAGAGGGTGTGAATCTCTCTCTGCTTCTTCAATGGCATACAAGGACCGGTGCCAGT 557
Db 644 TGAAGGACCAAGGGGTAAACTCTCTCTGCTGTACATGGCTTTCAAGATCGGTTCAGC 703
QY 558 GCAGCCACAGCCAGATGTACGAGATCTTCAGCATCATCCGGGACCTGGGGGCTTGGCCC 617
Db 704 TGACGGATTCACAGATCTATGAAGTACTGAGCGTGTATCCGGGATATTGGTCCATAGCTC 763

Db 249 TCCAGATGCCCTGACACAGGAAATGACATCCGCTGATGACTTCTTCCAGGGAACCAAGGCGG 308
Qy 318 CGCTAGCAGGAGGAAACCAACATGATCTTTGGACACAGCTCTTCCCCGACACAGCGGTGTAGCC 377
Db 309 CCCTGGCCGGGGGAAACCAACATGATCATGACCATGTTGTTCTTGAGCCCGGGACGAGCC 368
Qy 378 TGTGGCGGCTTACGAGAGTGGCGGAGCGGGCGGACAGCGCGCTGTCTGCGACTACT 437
Db 369 TATTGGCTGCTTTTGATCAGTGGAGGAGTGGGCTGACAGCAAGTCTCTGTGACTATT 428
Qy 438 CCCTGCACGTGGACATCACCCGATGGCATGAGACATCAAGGAGGAGCTGGAGCCCTGG 497
Db 429 CGCTGCACGTGGACATCACTGAGTGGCAAGGGCATCCAGGAGGAGATGGAAGCTCTGG 488
Qy 498 TCAAGGAGAGAGGCTGTGAATCTCTCTCTGCTCTTCAATGGCATACAAGGACCGGTGCCAGT 557
Db 489 TGAAGGACCAACCGGGTAACTCTCTCTCTGATGATGCTCTTCAAGATGATTCACGC 548
Qy 558 GCAGCGACAGCGATGATGAGATCTTCAAGATCATCTCGGACCTGGGGCCCTTGGCCC 617
Db 549 TGACGGATTCCTCAGATCTATGAGTGTGAGCGGTGATCCGGGATATCGGTGCCATGCTC 608
Qy 618 AGGTGCACGTGGAACCGGGACATCGTGGAGGAGGACAGAGCGGTTGCTGGAGCTCG 677
Db 609 AAGTCCACCGAGAGAAATGGTGACATCATGCTGAGGACACAGCAGAGGATCTCTGATCTGG 668
Qy 678 GCATCACTGGCCCGGAGGACATGCTCTCAGCCACCCCGGAGGAGGTGGAGGCTGAGGCGG 737
Db 669 GCATCAAGCGCCCGGAGGACATGCTGTTGAGCCCGGACAGAGGAGGTGAGGCTGAGCTG 728
Qy 738 TGTACCGAGCTGTACATCGCCAAAGCAGGAAATCGCCGCTGTAGCTCACCAGGTGA 797
Db 729 TGAACCGGTCCATCACTATTGTCACCAACAGACCAACTGCCCTCTGTATGTCAACAAAGTGA 788
Qy 798 TGAGCAAGGGGGCGGCGGACATCGCTCAGCCCAAGCCAGGAGGAGGTGGTGTGTTTG 857
Db 789 TGCCCAAGAGTGGCGCTGAAATCATGCTCAGGACCGGAAGAGGGAACCTGTGGTGTATG 848
Qy 858 GGGAGGCCATCAGCCGAGCTGGGCACCGACGCTTCACTACTGAGCAAGAACTGGG 917
Db 849 GTGAGCCCATCAGGCGCAGCTGGGAGCTGATGGCTCTGATTACTGGAGCAAGACTGGG 908
Qy 918 CCAAGGTGAGCCTTGTGTCATCACTACCCCTGTCAACCCAGACCCCAACCCAGCGAGCC 977
Db 909 CCAAGGTGCGGCTTGTGTCATCTCCCACTTGGAGCCCGGACCAACCACTCCAGACT 968
Qy 978 ACCTCACTGCTGCTGTCAGCGGGGACCTTCAAGGTGACAGGAGCGCCCACTGCACTT 1037
Db 969 TTCTCAACTGCTGCTGCTGTCAGAGACCTTCAAGTCACTGGCAGTGGCCCACTGCACTT 1028
Qy 1038 TCACCACTGCGCAGAGGCTGTGGGCAAGGACCAACTTTCGGCTGTATCCCGGAGGCAACCA 1097
Db 1029 TCAACACTGCGCAGAGGCTGTGGGAGGAGCAACTTTCACCTTGTTCGGAGGGGACCA 1088
Qy 1098 ACGGCAATTGAGGAGCGCATGTCGATGCTCTGGAGAAATGTGGCTCTTGGGAAGATGG 1157
Db 1089 ACGGCACTGAGGAGCGCATGCTGTCATTTGGGATAAGCTGTGGTCACTGGGAAGATGG 1148
Qy 1158 ACCAGATGATGCTGTCGCGGTGACCGATCAAAATGTCGCAAAATCTTCAATTTTACC 1217
Db 1149 ATGAGAATCAGTTTGTGGCTGTGACCAAGCAGCAACCAAGCTCTTCAACTTTTACC 1208
Qy 1218 CAAGGAAGGGCGAGTGGCTGTGGGCTTTCAGCTGACCTGCTGATATGGAACCCCAAGG 1277
Db 1209 CCGGGAAGGTGCGATCTCGTGGGATCTGATCTGACTTGGTCACTTGGGACCTTGACA 1268
Qy 1278 CCACCAAGATCACTCTTCCCAAGACCCCAATCTGAACTGGAGTACAACATCTTCCAGG 1337
Db 1269 GTGTGAAGACCACTCTCTGCCAAGACACACACAGTGTCTTGGATACACATCTTTGAAG 1328
Qy 1338 GAGTGAGTGCCTGGGAGCGCTTGGCGTGTGATTAAGTCAAGGCCGAGTGGCGCTCGAGG 1397

Db 1329 GCATGAGAGTGTGCGGGCTCCCCACTGGTGTGTCATCAGCCAGGGCAAGATTGTCTGGAGG 1388
Qy 1398 ACCGGAGAGATGTTTGTTCACCCCGGGCGGCGCTTCGTCCCTCGGAAACATTTCCCGG 1457
Db 1389 ACGGCACACTTTCATGTCTACATGAGGCTCAGAGGCTACATTTCCCGGAGCCCTTCCCTG 1448
Qy 1458 ACTTTGTCTTACAAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGGTGTGCCCC 1517
Db 1449 ACTTTGTGTACAAACGCATCAAGCAAGGAGCAGGCTGGCTGAGCTGAGAGGGTCCCTC 1508
Qy 1518 GTGGGCTGTATGAGCGGCCCGTCCACGAGTGTATGCTGCTGCGCAAGCCAGGAGTGGCG 1577
Db 1509 GTGGCTGTATGAGCGGACCGGTATGCGAGGTGTCTGTGACGCCCAAGACGCTGACTCCAG 1568
Qy 1578 CTCCGGCCCGCGCTCTGCCAGGCAAGATCTCCGTGCTCTGTGCGCAACCTACATC 1637
Db 1569 CCTCATCAGCTAAGACATCCCTTCCAGCAGCAGGACCACTTGTTCGGAACCTGCACC 1628
Qy 1638 AGTCGGGTTTACGCTTATCTGGGTCTCAGGCTGATGATCAACATCGCCCGGACGC 1690
Db 1629 AGTCGGATTGAGTGTCTGTGCTCAGATTGACGACAACTTTCCCGCGCGC 1681

RESULT 11

ABK91188
ID ABK91188 standard; cDNA; 1829 BP.

XX ABK91188;

DT 05-NOV-2002 (first entry)

XX Human cDNA encoding Ulip2/CRMP2 protein.

DE Human; ss: gene; Ulip2; CRMP2; collapsin response mediator protein;
XX Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;
KW paraneoplastic neurodegenerative disease; PND; myelination;
KW demyelination; remyelination; myelin disorder; multiple sclerosis;
KW autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;
KW human T lymphocyte virus 1.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 72..1793
CDS /*tag= a
FT /product= "Ulip2/CRMP2"
FT

XX US2002119944-A1.

XX 29-AUG-2002.

XX 09-NOV-2001; 2001US-00986632.

XX 09-NOV-2000; 2000US-0246751P.

XX (AGUE/) AGUERA M.

XX (BELI/) BELIN M.

XX (CHAR/) CHARRIER E.

XX (HONO/) HONORAT J.

XX (RICA/) RICARD D.

XX (ROGE/) ROGEMOND V.

XX Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;

XX WPI; 2002-627172/67.

XX P-PSDB; ABG32228.

XX Prevention or treatment of myelin disorders, such as multiple sclerosis,

XX by administering an agent selected from a Ulip/CRMP protein, a nucleic

XX acid coding for the protein, or an antibody directed against protein.

XX Claim 14; Page 17-18; 44pp; English.

The invention relates to a new method for prevention or treatment of myelin disorders, comprises administering to a patient an effective amount of an agent selected from a Ulp1 (Unc-33-like protein)/CRMP (collapsin response mediator protein) protein, a nucleic acid coding for Ulp1/CRMP, an antisense sequence capable of specifically hybridizing with the nucleic acid, an antibody directed against Ulp1/CRMP, or an aptamer capable of binding Ulp1/CRMP, and a pharmacologically acceptable carrier. Also included are methods of diagnosing a myelin disorder in a subject, identifying agents useful for the prevention or treatment of myelin disorders, using the Ulp1/CRMP proteins/nucleic acids, agents capable of modulating the function or expression of the proteins (increasing or decreasing), and a method for identifying an endogenous agent as a therapeutic target for the prevention or the treatment of myelin disorders. The agents are useful for preventing or treating a myelin disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus 1) associated myelopathy and neurodegenerative diseases, Alzheimer's disease, paraneoplastic neurodegenerative diseases (PND), autoimmune neurodegenerative disorder. Ulp1/CRMP proteins are involved in the processes of myelination, demyelination and remyelination. Antibodies to a Ulp1/CRMP protein are useful for diagnosing a myelin disorder. The present sequence encodes Ulp12/CRMP2 protein

SQ Sequence 1829 BP; 426 A; 509 C; 511 G; 383 T; 0 U; 0 Other;

Query Match 57.1%; Score 965.4; DB 6; Length 1829;
Best Local Similarity 73.6%; Pred. No. 3.1e-188;
Matches 1230; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 20 CCAGAGCAGGATGCTCTTCCAGGCGAAGAAAGCATCCCCGGATFCAGAGTACCGC 79
DB 60 CCAGAGCAGGATGCTTATCAGGCGAAGAAATATTCACGCGATCAGAGCGATCGT 119
QY 80 CTTCTGATCAGAGTGGGAGTCTGATGACGACGAGCTCTTTACGCTGATGTCAC 139
DB 120 CTTCTGATCAAGGAGGTAAATTTGTAATGATGACGAGCTGTCTATGACAGATATC 179
QY 140 GTGCAAGATGGCTTGAATAAATCGGAGAAACCTCATCGTCCCTGGGGGCATCAAG 199
DB 180 ATGGAAGATGGTTGATCAAGCAATAGGAAATCTGATGTGCCAGAGAGTGAAG 239
QY 200 ACCATTGACGCCACCGCTGATGGTCTCTTCTGGTGGGCTTGAAGTCCACAAAGCTG 259
DB 240 ACCATCGAGGCCACTCCCGGATGGTGTATCCCGAGGAATTCAGCTCCACACTCGTTTC 299
QY 260 CAGATGCTGCTCGGCGATGACACCGCTGACGACTTCTGTGAGGGCACCAGGACGG 319
DB 300 CAGATGCTGATCAGGGAATGACGCTGCTGATGATTTCTTCAAGGAACTCAAGGGCGCC 359
QY 320 CTAGCAGGAGGAACCATGATCTTGGACACAGTCTTCCCGACACAGGCTGTGAGCTG 379
DB 360 CTGGCTGGGGAAACCATATGATCATTTGACCATGTTGTTCTGAGCCTGGGACAGCCTG 419
QY 380 CTGGCGGCTTACGAGCAGTGGCGGAGCGGGCGGACAGCGCGCTCTGCGACTACTCC 439
DB 420 CTCGCTGCTTTGACCACTGGAGGAATGGGCGGACAGCAAGTCTCTGTGACTACTCT 479
QY 440 CTGCACTGACATACCCGATGGCATGAGAGCATCAAGGAGAGCTGGAGGCGCTGGTC 499
DB 480 CTGCATGTGGACATCAGCGAGTGGCATTAAGGGCATCCAGGAGAGATGGAAGCGCTTGTG 539
QY 500 AAGGAGAGGGGTGAACTCTTCTGGTCTTCTGATGATGATGATGATGATGATGATGATG 559
DB 540 AAGGATCAAGGGTAAATCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 599
QY 560 AGCGACAGCAGATGATACGAGATCTTTCAGCATCATCCGGACCTGGGGGCTTTGGCCAG 619
DB 600 ACGGATTCAGATTTATGAATGATGATGATGATGATGATGATGATGATGATGATGATG 659
QY 620 GTGCACTGACAGAGGAGCATGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 679
DB 660 GTCCAGCAGAAATGGCGACATCATTTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
QY 680 ATCACTGGCCCCGAGGGCCACGCTGCTCAGCCACCCCGAGGAGGTGGAGGCTGAGGGCGTGTG 739

RESULT 12
ACF25352
ID ACF25352 standard; DNA; 4459 BP.
XX
AC ACF25352;

DB 720 ATCAGGGGCGCGAGGAGCATGTGCTGAGCGAGCATGTGAGGAGGCTGAGGCGCGGCTG 779
QY 740 TACCGAGCTGTACCATCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 799
DB 780 AATCGTGCATCACCATCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 839
QY 800 AGCAAGGGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 859
DB 840 AGCAAGGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 899
QY 860 GAGCCCATCACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 919
DB 900 GAGCCCATCACCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959
QY 920 AAGGCTGAGCCTTGTGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 979
DB 960 AAGGCTGCTGCTTGTGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019
QY 980 CTCACCTGCTGCTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1039
DB 1020 CTCACCTGCTGCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1079
QY 1040 ACCACTGCCCCAGAGGCTGTGGGCAAGGAGCAACTTGGCGCTGATCCCCGAGGAGGAGGAG 1099
DB 1080 AACACTGCCCCAGAGGCTGTAGGAAAGGAGCAACTTCACTGATTCGGGAGGAGGAGGAG 1139
QY 1100 GGCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1159
DB 1140 GGCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199
QY 1160 GAGATGAGTCTGCTGCGGCTGACAGTCAAAATGCTGCCAAATCTTCAATTTTACCCCA 1219
DB 1200 GAGAACCAATTTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1259
QY 1220 AGGAAAGGCGGAGTGGCTGTGGGCTGTGACCTGACCTGCTCATATGGAACCCCAAGGCG 1279
DB 1260 CGGAAAGGCGGATGCTGTGGGATCCGATCCGACCTGCTCATCTGGGAGCCCGGACAGC 1319
QY 1280 ACCAAGATCATCTGCGCAAGACCCCAATCTGAAAGTGGAGTACAAATCTTCGAGGGA 1339
DB 1320 GTTAAACCATCTCTGCGCAAGACACACACAGCTCTCTCGAGTACAAATCTTTGAAGGC 1379
QY 1340 GTGGAGTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1399
DB 1380 ATGGAGTGGCGGCTTCCCACTGCTGGTGTGATGAGCCAGGAGGAGGAGGAGGAGGAGG 1439
QY 1400 GGGAGATGTTGTTCACCCCGGGGCGGCGCTTCTGCTCCCTCGGAAAAACATTTCCCGGAC 1459
DB 1440 GGCACCTGCTGATGACCGAGGCTCTGGAAGCTATATTTCCCGGAGGAGGAGGAGGAGG 1499
QY 1460 TTTGTCTCAAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGGTGTGCGCGCT 1519
DB 1500 TTTGTCTCAAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGGTGTGCGCGCT 1559
QY 1520 GGGCTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1579
DB 1560 GGGCTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1619
QY 1580 CCGGCGCGGCGCTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1639
DB 1620 TCTCGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1679
QY 1640 TCGGGGTTGAGGCTATCTGGGCTGAGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1690
DB 1680 TCTGGATTCAGGTTGTCTGGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1730

XX DT	22-SEP-2003 (first entry)	Db	623	CTCGCTGCTTTTGAACCAAGTGAAGGAAATGGCCGACAGCAAGTCTCTGCTGACTACTCT	682
XX DE	Human dihydropyrimidinase-related protein gene.	Qy	440	CTGCAGTGGACATCAACCCGATGAGCATCAAGAGGAGCTGGAGGCGCTCGGTC	499
XX KW	spinal cord; neuropathic pain; central sensitisation pain; pain;	Db	683	CTGCATGTGGACATCAGCGAGTGGCATAGGGGATCCAGGAGGAGATGGAGGCTTGTG	742
XX KW	analgesic; gene therapy; gene; ss.	Qy	500	AAGGAGAGGGTGTGAATCTCTTCTTCTGCTTCTCATGGCATACAAGGACCGGTGCAAGTC	559
XX OS	Homo sapiens.	Db	743	AAGGATCACGGGGTAAATTCCTTCTCTGCTGTAATGGCTTTCAAGATCGCTTCCAGCTA	802
XX PN	EPI284298-A2.	Qy	560	AGGACAGCCAGATGTACGAGATCTTCAGCATCATCGGACCTGGGGCTTGGGCCAG	619
XX PD	19-FEB-2003.	Db	803	ACGATTTGCCAGATTTATGAGTACTGAGTGTGATCGGGATATGGCGCATAGCCAA	862
XX PF	26-JUL-2002; 2002EP-00255229.	Qy	620	GTGCACGCTGAGAAACGGGGACATCTGTGAGGAGGAGCAGAGCGTGTGTGAGTCTGGC	679
XX PR	27-JUL-2001; 2001GB-00018354.	Db	863	GTCCACGTCAGAAATGGCGACATCATTTGCAGAGGAGCAGCAGAGGATCTCTGGATCTGGGC	922
XX PR	07-FEB-2002; 2002GB-00002883.	Qy	680	ATCATCTGGCCCGAGGGCCACGTGCTCAGCCACCCGAGAGGTGAGGCTGAGGGCGTG	739
XX PA	(WARN) WARNER LAMBERT CO.	Db	923	ATCACGGGGCCCGAGGGACATGTGCTGAGCGGACCTGAGGAGGTGAGGCGGAGCGGTG	982
XX PI	Brookebank RA, Dixon AK, Lee K, Pinnock RD;	Qy	740	TACCGAGCTGTACCATCGCCAGGAGGCAAACTGCCCGCTGTACCTCACCAGAGGTGATG	799
XX DR	WPI; 2003-543489/52.	Db	983	AATCGTGCCATCACCATCGCCAAACAGACCAACTGCCCGCTGTATATCACCAAGGTGATG	1042
XX DR	N-PSDB; ACP25353.	Qy	800	AGCAAGGGGGCGCCGACGCTCATGCTCAGGCCCAAGCGCAGAGGGGTGGTGTGTTGGG	859
XX PT	Use of an isolated gene sequence in the screening of compounds for	Db	1043	AGCAAAAGCTCTGCTGAGGTCTATCGCCAGGACCGAAGAGGAACTGTGTGTATGGC	1102
XX PT	diagnosing or treating pain.	Qy	860	GAGCCCATCAACCGCCAGCTTGGGCAACCGACGGTTCACTATCTGAGAGCAAGAACTGGGCC	919
XX PS	Claim 1; Page 99-100; 188pp; English.	Db	1103	GAGCCCATCACTGCGACGCTTGGGAACGGACGGCTCCCATTTACTGTGAGCAAGAACTGGGCC	1162
XX CC	The invention relates to a novel isolated gene sequence that is	Qy	920	AAGGCTGACAGCTTCTGTCAATCACCCCTGTCTCAACCCAGAGCCCAACCCAGGAGCCAC	979
XX CC	downregulated in the spinal cord of a mammal in response to mechanically	Db	1163	AAGGCTGCTGCTTGTCTCACTCCCTCCACCTTGGAGCCCTGATCAACCACTCCAGACTTT	1222
XX CC	distinct first and second models of neuropathic or central sensitisation	Qy	980	CTCACCTGTGTGTCAGCGGGGACCTCCAGGTGACAGGAGGAGCGCCACTGACCTTC	1039
XX CC	pain, useful in the screening of compounds for diagnosing or treating	Db	1223	CTCACTCTCTGCTGCTGTGAGAGCTTCAGGTCAAGGAGTGGCCATTTGACAGTTT	1282
XX CC	pain. A protein encoded by a gene of the invention has analgesic	Qy	1040	ACCACTGCCAGAAAGCTGTGGGCAAGGACAACTTCGCGCTGATCCCGAGGAGCAACAAC	1099
XX CC	activity. A polynucleotide of the invention may have a use in gene	Db	1283	ACACTGCCAGAAAGCTGTAGGAAAGGACAACTTCACCTGATTCGAGAGGACCAAT	1342
XX CC	therapy. The gene sequence is useful for preparing a composition for	Qy	1100	GGCAITTGAGAGGCGCATGTGATGCTGTGGAGAAATGTGTGCTCTGGAGAGATGGAC	1159
XX CC	diagnosing or treating pain. The present sequence represents a gene of	Db	1343	GGCACTGAGAGGCGGATGTCCGTCATCTGGGACAAAGGCTGTGTGCTCACTGGGAAAGTGGAT	1402
XX CC	the invention	Qy	1160	GAGAAATGAGTTCTGTCGCGGTGACCAAGTACAAATGTGCGCAAAATCTTCAATTTTACCCA	1219
XX SQ	Sequence 4459 BP; 1074 A; 1086 C; 1047 G; 1252 T; 0 U; 0 Other;	Db	1403	GAGAACAGTTGTGTGCTGTGACCAAGCAACATGAGCCAAAGTCTTCACTTTACCCC	1462
	Query Match 57.0%; Score 963.8; DB 9; Length 4459;	Qy	1220	AGGAAAGGCGAGTGTGCTGTGGCTCTGACGCTGACCTGTGTATATGGAACCCCAAGGCC	1279
	Best Local Similarity 73.5%; Pred. No. 7.6e-188;	Db	1463	CGGAAAGGCGCATTTCTGTGGGATCCGATCCGACCTGTGTCTATCTGGAGCCCGCAGC	1522
	Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;	Qy	1280	ACCAAGATCATCTCTGCCAAGACCCCAATCTGAACGTGGAGTACAACATCTTCGAGGGA	1339
Qy	20 CCCAGGAGCAGGATGTCTCTCCAGGGCAAGAAAGCATCCCCGGATCAGAGTGACCGC	Db	1523	GTTAAACCATCTCTGCCAAGACACACACAGCTCTCTCGAGTACAACTCTTTGAAGGC	1582
Db	263 CCCAGGAGAGAGATGTCTTTATCAGGGGAGAGAAATATTCACGCATCAGAGCGATCGT	Qy	1340	GTGGAGTGGCGGAGCGCTGCGGTGTCTAAGTCAAGGCGAGTGGCGCTGGAGGAC	1399
Qy	80 CTTCGTGATCAGAGGTGGAGGATCGTCAATGACACAGTCTTTTACGCTGATGTGCAC	Db	1583	ATGGAGTGGCGGCTTCCCACTGTGTGTGTATCAGCCAGGGAGAGTTGTCTCTGGAGGAC	1642
Db	323 CTTCGTATCAAGAGGAGTAAATTTTATGATGACCAAGTGTCTATGACAGATATAC	Qy	1400	GGGAAAGATGTTGTCAACCCCGGGCGGCGCTTCTGTCTCTCGAAAAATTCCTCCGGAC	1459
Qy	140 GTGGAAGATGGCTTTGATAAAACAAATCGAGAAACCTCATCGTCCCTGGGGGATCAAG	Db	1643	GGCACCTCTGATGTCAACCGGAGGCTCTGGAGCGCTACATTTCCCGGAGGCCCTTCCCTGAT	1702
Db	383 ATGGAGATGGTTGATCAAGCAATAGGAGAAATCTGATTTGCCAGAGGAGTGAAG	Qy	1460	TTTGTCTACAGAGGATCAAGAGCTCGCAACAGGCTGGCGGAGATCAACGCTGTGTCGCCGT	1519
Qy	200 ACCATTAGCCGCAACGGCTGATGGTCTTCTGCTGGCGGTGTGACGTCCAACAGGCTG	Db	1703	TTTGTTTTACAAGCGTATCAAGGCAAGGAGCAGGCTGGCTGAGCTGAGAGGGGTTCCTCGT	1762
Db	443 ACCATCAGGCGCCACTCCCGATGGTGTATCCCGAGGAAATGACGTCCAACACTCGTTTC				
Qy	260 CAGATGCTCTGTCGGGATGACACCGCTGACGACTTCTGTGAGGCGACCAAGGACGCG				
Db	503 CAGATGCTGATCAGGGAATGACGTCTGCTGATGATTTCTTCAAGGAAACCAAGCGGCGC				
Qy	320 CTAGCAGGAGAACCACTATGATCTTGGACACAGCTCTTCCCGGACAGCGGTGTGAGCTG				
Db	563 CTGGCTGGGGACCACTATGATCATTTGACCAAGTGTCTTCTGAGCTTGGGACAGGCTG				
Qy	380 CTGGCGGCTTACAGAGCATGTGGCGGAGCGGCGGACAGCGCGCTGCTCGACTACTCC				

QY 1520 GGGCTGTATGACGGGCCCGCTCCACGAGGTGATGGTGCCTGCCAAGCCAGGAGTGGGCT 1579
DB 1763 GGCTGTATGACGAGACTGTGTGAGTGTCTGTGAGCGCCCAAGACAGTCACTCCAGCC 1822
QY 1580 CCGGCCCGCGCGCTCTCCAGGCAAGATCTCCGTGCTCTCTGTGGCCAACTTACATCAG 1639
DB 1823 TCCTCGGCCAAGAGTCTCTGCCAAGCAGCAGGCCCACTGTCCGGAACCTGACACAG 1882
QY 1640 TCGGGGTTGAGCCATCTCTGGGTCTCAGGCTGATGACACATCCGCCGACGC 1690
DB 1883 TCTGGATCAGTTGTCTGTGGTCTCAGATTGATGACAACTTCCCGCCGC 1933
RESULT 13
ADC66333
ID ADC66333 standard; DNA; 4459 BP.
XX AC ADC66333;
XX DE 18-DEC-2003 (first entry)
XX DT Human collapsin response mediator protein 2 gene 3' UTR sequence.
XX DE neuroprotective; nootropic; neuroleptic; gene therapy;
XX KW human collapsin response mediator protein 2; neurodegenerative disease;
XX KW Alzheimer's disease; Down syndrome; schizophrenia; H-ras; ds.
XX OS Homo sapiens.
XX XX W02003040320-A2.
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002MO-US035323.
XX PR 08-NOV-2001; 2001US-00006911.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Gaarde WA, Watt AT;
XX WP1; 2003-449447/42.
XX PT New compound, having a sequence targeted to a nucleic acid encoding human
PT collapsin response mediator protein 2, useful for preparing a composition
PT for treating neurodegenerative disease, e.g., Alzheimer's disease.
XX PS Example 15; SEQ ID NO 11; 102pp; English.
XX CC The invention relates to a new compound having a sequence comprising 8-50
CC bp targeted to a nucleic acid encoding human collapsin response mediator
CC protein 2 which specifically hybridizes with the nucleic acid encoding
CC human collapsin response mediator protein 2 and inhibits its expression.
CC The compound is useful for preparing a composition for treating
CC neurodegenerative disease, e.g., Alzheimer's disease, Down syndrome or
CC schizophrenia. This sequence represents the human collapsin response
CC mediator protein 2 gene 3' untranslated (3'UTR) sequence against which
CC the antisense oligonucleotides may be targeted.
XX SQ Sequence 4459 BP; 1074 A; 1086 C; 1047 G; 1252 T; 0 U; 0 Other;
Query Match 57.0%; Score 963.8; DB 10; Length 4459;
Best Local Similarity 73.5%; Pred. No. 7.6e-188;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;
QY 20 CCAGGAGCAGGATGTCTTCCAGGGCAAGAAAGCATCCCGGATCAGGATGACCGC 79
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DB 323 CTTCTGATCAAGAGGAGTAAATTTGTTAATGATGACCAAGTCTTATGCAGACATATAC 382

QY 140 GTGGAGATGGCTTGATATAAAACAATCGAGAAAAACCTCATCGTCCCTGGGGGCATCAAG 199
DB 383 ATGGAGATGGGTGTGATCAAGCAAAATAGAGAAAATCTGATTTGTCAGGAGAGATGAAG 442
QY 200 ACCATTGACGCCCAAGCCCTGATGGTCTCTTCTGGTGGGTTGAGCTCCACAAGGCTG 259
DB 443 ACCATCGAGGCCCACTCCCGGATGTGATCCCGGAGGAATTTGACGTCCACACTCGTTTC 502
QY 260 CAGATGCTGTCTCTGGGCATGACACCGGCTGACGACTTCTGTACGGGCACCAAGGACGG 319
DB 503 CAGATGCTGTGATCAGGGAATGACGCTGTGCTGATGATTTCTTCCAAAGAAACCAAGCGCGC 562
QY 320 CTAGCAGGAGGAACCAACCATGATCTTGGACCACTCTTCCCGGACACGGGTGTGACCTG 379
DB 563 CTGGCTGGGGGAACCACTATGATCATTTGACCACTGTGTTCTTGAGCTCGGACCAAGCTTC 622
QY 380 CTGGCGGCTTACGAGCAGTGGCGGAGCGGGGAGCAGCGCGCTCTGTCGCACTACTCC 439
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DB 743 AAGGATCACGGGGTAAATTCCTTCTCTGCTGTGATACATGGCTTTCAAGATCGCTTCCAGCTA 802
QY 560 AGCGACAGCAGATGTACAGATCTTTCAGCATCATCCGGGACCTTGGGGGCTTGGGCCAG 619
DB 803 ACGGATTGCCAGATTTATGAGTACTGAGTGTGATCCGGGATATTGGCGCCATAGCCCCAA 862
QY 620 GTGCACGCTGGAACCGGGACATCTGTGAGGAGGAGCAGAACGGTGTCTGAGACTCGGC 679
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DB 923 ATCAGGGGCCCGAGGGAATGTTGCTGAGCCGACCTGAGGAGGTGAGGCCCAAGCCGTG 982
QY 740 TACCGAGCTGTCAACATCCCAAGCAGGCAAACTTGCCCGCTGTAGCTCACCAAGGTGATG 799
DB 983 AATCGTGCCATCACCATCCCAACACAGACCAACTGCCCGCTGTATATACCAAGGTGATG 1042
QY 800 AGCAAGGGGGCGGCGACGCCATCTGCTCAGGCCAAGCGCAGAGGGGTGTGTTGGG 859
DB 1043 AGCAAAAGCTCTGCTGAGGTCTATCGCCAGGCAAGGAGGAACTGTGTGTATGGC 1102
QY 860 GAGCCCATCACCGCAGCCTGGGCAACCGAGGTTTACACTTCTGGAGCAAGAACTGGGCGC 919
DB 1103 GAGCCCATCACTGCCAGCTTGGGAACGGACGGCTCCCATTTACTTGGAGCAAGAACTGGGCGC 1162
QY 920 AAGGCTGACGCTTCTGTACATCACCCCTGTCAACCCAGACGCCACCAAGCAGGACCAAC 979
DB 1163 AAGGCTGCTGCTTTGTGACCTCCCACTCCCACTTGGAGCCCTGATCCACCACTCCAGACTTT 1222
QY 980 CTCACCTGTTGCTGTCCAGCGGGACCTTCCAGGTGACAGGAGCGGCCCACTGCACTTC 1039
DB 1223 CTCACCTGCTGTGCTGTGAGACCTCCAGGTCAAGGAGCTCCAGGTCAAGGAGTGGCACTT 1282
QY 1040 ACCATGCCCCAGAGGCTGTGGCAGGACAACTTTCGCGCTGATCCCGGAGGACCAAC 1099
DB 1283 AACACTGCCCAAGAGGCTGTAGGAAAGGACAACTTCAACCTGATTCGGAGGGGACCAAT 1342
QY 1100 GGCAATTGAGAGCGCATGTGATGGTCTGGGAGAAATGTGTGGCTCTCTGGGAGATGGAC 1159
DB 1343 GGCACTGAGAGCGGATGTCCGTCTATCTGGACAAAGGCTGTGGTCACTGGGAGATGGAT 1402
QY 1160 GAGAAATGATTTGCTCGCGGTGACCAAGTACAAATGTCTGCCAAAATCTTCAATTTTACCCA 1219
DB 1403 GAGAACCAAGTTGTGGCTGTGACCAAGCAATGACCAAAAGTCTTCAACCTTTACCCC 1462

Qy 1220 AGGAAGGGGCGAGTGGGCTTGAGCGCTGACCTGTGATATATGAAACCCCAAGGCC 1279
Db 1463 CGGAAGGCGCGCATTTGCTGTGGATCGGATCGGACCTGTGCTATCTGGGACCCGACAGC 1522
Qy 1280 ACCAAGATCATCTCTGCCAAGACCCACAACTGAACTGAGTACACATCTTCGAGGGA 1339
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Qy 1340 GTGAGTCCGCGGAGCGCTCGCCGTGTCTATAGTCAAGGCGCGAGTGGCGCTGGAGGAC 1399
Db 1583 ATGGAGTCCGCGGCTCCCACTGCTGTGTCATCAGCCAGGGGAAGATTTGCTCTGGAGGAC 1642
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Qy 1460 TTTGTCTACAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGCTGTGCCCGT 1519
Db 1703 TTTGTTTACAGCGTATCAAGGCAAGGACGAGCGGCTGGCTGAGCTGAGAGGGGTTCTCGT 1762
Qy 1520 GGGCTGTATGACGGGCGGCTGTCACAGGTGATGCTGCTGCTGCCAAGCCAGGGAGTGGCGCT 1579
Db 1763 GGCCTGTATGACGGACCTGTGTGTGAGTGTCTGTGAGCGCCCAAGACAGTCACTCCAGCC 1822
Qy 1580 CCGGCGCGCGCTCTGCCAGGCAAGATCTCCGTGCTCTCTGTGCGCAACCTATACATCAG 1639
Db 1823 TCCTCGGCCAAGAGCTCTCTGCGCAAGCAGCAGCGCCCACTGTGCGGAACCTGCAACAG 1882
Qy 1640 TCGGGGTTACGCTATCTGGGTCTCAGGCTGATGACCAACATCGCCGAGCC 1690
Db 1883 TCTGGATTGATTTGTCTGGTGTCTCAGATTGATGACAAACATTTCCCGCGCC 1933

RESULT 14

ADR98995 standard; DNA; 4459 BP.
XX ADR98995;
AC AC
XX 02-DEC-2004 (first entry)
DT DT
XX Dihydropyrimidinase-like 2, DPYSL2, coding sequence, SEQ ID 1.
DE DE
XX Cytostatic; breast cancer; cancer; human; gene; ds;
XX Dihydropyrimidinase-like 2, DPYSL2.
KW KW
XX Homo sapiens.
OS OS
XX WO2004078035-A2.
PN PN
XX 16-SEP-2004.
XX 27-FEB-2004; 2004WO-US007268.
XX 28-FEB-2003; 2003US-0450655P.
XX (FARB) BAYER PHARM CORP.
XX
XX Eveleigh D, Bigwood D;
XX WPI; 2004-653556/63.
XX P-PSDB; ADR99122.
XX REFSEQ; NM_001386.1.
XX
XX Diagnosing breast cancer comprises comparing the level of expression of
PT genes or gene products in a first biological sample taken from a patient
PT with that in a normal patient sample.
XX
XX Claim 2; SEQ ID NO 1; 53pp; English.
PS PS
XX The present invention relates to a method (M1) for diagnosing breast
CC cancer in a patient. The method comprises comparing the level of
CC expression of one or more genes or gene products in a biological sample

CC from the patient with that in a normal patient sample, where a difference
CC in the gene expression in the first sample compared to that in the second
CC sample is a diagnostic of the disease. Also claimed are: method (M2) for
CC distinguishing between normal and disease tissues; method (M3) for
CC monitoring the response of a breast cancer patient to treatment with an
CC anti-cancer agent; method (M4) for identifying a compound for treating
CC breast cancer; and an array for distinguishing between normal and disease
CC tissues comprising two or more probes corresponding to genes selected
CC from ADR98995-ADR99121 or comprising two or more polypeptides selected
CC from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995
CC -ADR99121 and the gene products are polypeptides selected from ADR99122-
CC ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are
CC useful for distinguishing between normal and disease tissue. M3 is useful
CC for monitoring the response of a breast cancer patient to treatment with
CC an anti-cancer agent. M4 is useful for identifying a compound for
CC treating breast cancer. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 4459 BP; 1074 A; 1086 C; 1047 G; 1252 T; 0 U; 0 Other;

Query Match 57.0%; Score 963.8; DB 13; Length 4459;
Best Local Similarity 73.5%; Pred. No. 7.6e-188;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

Qy 20 CCAGGAGCAGGATGTCCTTCCAGGCAAGAAAGCATCCCCGGATCAGAGTGACCGC 79
Db 263 CCAGGAGGAGATGTCCTTATCAGGGGAAGAAAATATTCACGATCAGAGCGATCGT 322
Qy 80 CTTCTGATCAGAGTGGGAGATCGTGAATGACGACAGTCTTTTACGCTGATGTGCAC 139
Db 323 CTTCTGATCAAGAGGTTAAATTTGTAATGATGACCACTCGTTCTATGCAGACATATAC 382
Qy 140 GTGGAAGATGGCTTGATATAAAACAAATCGGAGAAACCTCATCGTCCCTGGGGCATCAAG 199
Db 383 ATGGAAGATGGGTTGATCAAGCAATAGGAGAAATCTGATTTGCCAGGAGGATGAAG 442
Qy 200 ACCATTGACGCGCCACGCGCTGATGTCCTTCTGTGGGCTTGACCTGCCACACAAGGCTG 259
Db 443 ACCATCGAGGCCACATCCCGGATGGTGATCCCGGAGGAATTCACGTCACACATCGTTTC 502
Qy 260 CAGATGCTGTCTCGGCGATGACACCGGCTGACACTTCTGTAGGGGACCAAGGACGCG 319
Db 503 CAGATGCTGTATCAGGGAATGACGCTGTGCTGATGATTTCTTCCAAGGAACCAAGGGCGCC 562
Qy 320 CTAGCAGGAGGACCAACCATGATCTTGGACCACTCTTCCCGACACGCGGTGTGAGCCTG 379
Db 563 CTGGCTGGGGGAACCACTATGATCATTTGACCACTGTTGTTCTGAGCTGGGACAAGCCTG 622
Qy 380 CTGGCGGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGCGCTGCTCGACTACTCC 439
Db 623 CTGCTGCTTTGACCACTGGAGGGAATGGCGGACAGCAAGTCTCTGTGACTACTCT 682
Qy 440 CTGCACTGGACATCACCCGATGGCATGAGAGATCAAGAGAGCTGTGAGGCGCTGGTC 499
Db 683 CTGCACTGGACATCAGCGAGTGGCATAGGGGATCCAGGAGGATGGAAGCGCTGTG 742
Qy 500 AAGGAGAGGGTGTGAACCTCTTCTGCTTTCATGCGATACAGGACCGTTCGCGAGTGC 559
Db 743 AAGGATCAGGGGGTAAATTCCTTCTCGTGTATATGGCTTTCAAGATCGCTTCCAGCTA 802
Qy 560 AGCGACAGCCAGATGTACGAGATCTTTCAGCATCATCCGGGACCTGGGGGCTTGGGCCAG 619
Db 803 ACGGATTCAGATTTTATGAGTACTGAGTGTGATCGGGATATTGGCGCCATAGCCAA 862
Qy 620 GTGCACTGTGAGAACCGGGACATCTGTGGAGGAGGACAGAACGCTGTGTGAGCTGCGC 679
Db 863 GTCCACGACAGAAATGCGGACATCAATTGACAGAGGAGCAGCAGAGGATCCTGTGATCTGGC 922
Qy 680 ATCACTGGCCCCCGAGGCGCACGCTGCTCAGCCACCCCGAGGAGGTGAGGCTGAGGCGGTG 739
Db 923 ATCAGCGGCCCCGAGGACATGTGTGAGCCGACCTGAGGAGGTGAGGCGCGAAGCGGTG 982

to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 3447 sequences (given in ABU61564 to ABU70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate) or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' s tumour

SQ Sequence 5421 BP; 1390 A; 1269 C; 1209 G; 1553 T; 0 U; 0 Other;

Query Match	57.0%	Score 963.8	DB 6	Length 5421
Best Local Similarity	73.5%	Pred. NO. 7.8e-188		
Matches 1229	Conservative	0	Mismatches 442	Indels 0
			Gaps	0

Qy	20	CCCAAGACGAGATGTCCTTCCAGGGCAAGAAAAGCATCCCCCGGATACCGAGTGACGCG	79
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Qy	80	CTTCTGATCAGAGGAGGTAAATTTGTTAATGATGACGAGTCGTTCTATGCGAGACATATAC	1444
Db	1385	GTGGAAGATGGCTTTGTATAAACAAATCGGAGAAAACCTCATCGTCCCTCGGGGGCATCAAG	199
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		CAGATGCTGTCTGGGCGATCACACCGGCTGACGACTCTCTCAGGGGACCAAGGCGAGCG	319
Qy	260		1565
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		CTAGCAGGAGGAACCAACATGATCTTGGAACACGCTCTTCCCOCGACAGGGGTGTCAGCCGTG	379
Qy	320	CTGCTGGGGAAACCATATGATCATTTGACCAACGTTGTTCTTGAGCCTGGGACAGCCGTG	1684
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		CTCGCTGCTTTGACCAAGTGAGGGAATGGGCGGACAGCAAGTCCTGCTGTGACTACTCT	1744
Qy	440	CTGCACTGTGCATCACCCGATGGCATCAGAGCATCAAGGAGGAGCTGGAGGCCCTGGTC	499
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		AAGGAGAAGGGTGTGAACTCCTTCTGTGCTTTCATGGCATACAAAGGACCGGTGCCAGTGC	559
Qy	500	AAGGATCACGGGGTAAATTCCTTCTCGTGTACATGGCTTTCAAGATCGCTTCAGACTA	1864
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		ACGGATTTGCCAGATTTTATGAAGTACTGAGTGTGATCCGGGATATTGGCGCCATGACCCAA	1924
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Db	1925	GTCCACGACGAAATGGCGACATCATTTGCAGAGGACGACGAGGATCTCTGGAATCTGGGC	1984
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Search completed: September 24, 2005, 00:18:31
Job time : 3124 secs

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Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, K.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 4239)

Strausberg, R.

Direct Submission

Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps@remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mc@nhgri.nih.gov

Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 100 Row: 0 Column: 8

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753677

This clone has the following problem: retained intron.

Location/Qualifiers

1. 4239

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clones="IMAGE:6492897"

/tissue type="Eye, retina, mouse strain C57Bl/6"

/clone_id="NIH_MGC_94"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

FEATURES

source

ORIGIN

Query Match 55.5%; Score 937.8; DB 3; Length 4239;

Best Local Similarity 87.1%; Pred. No. 9.1e-200;

Matches 1029; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

Qy 509 GGTGTGAACCTCTTCCTGGTCTTCATGGCAATACAAAGACCGGTGCCAGTGACGACGAGC 568

Db 2153 GGTGTGAACCTCTTCCTGGTCTTCATGGCAATACAAAGACCGGTGCCAGTGACGACGAGC 2212

Qy 569 CAGATGTACGAGATCTTCAGCATCATCGGACCTCGGGGCTTGGCCCGAGGTGCAGCT 628

Db 2213 CAGATATATGAATCTTCAGCCTCATCGGAGCCTGGGAGCTGTGGCCCGAGGTGCAGCA 2272

Qy 629 GAGAACGGGGACATCGTGGAGGAGGAGCAGAACGGTTCCTGGAGCTCGGCATCAGCTGGC 688

Db 2273 GAAATGGGGACATCGTGGAGGAGGAGCAGAACGGTTCCTGGAGCAAGGCATCAGCTGGT 2332

Qy 689 CCCGAGGGCCACGCTGCTCAGCCACCCGAGGAGGTGGAGGCTGAGGGGCTGACCGAGCT 748

Db 2333 CCTGAGGGCCACGCTGCTCAGCCACCCAGAGAGGTAGAGCCGAGGCTGTGTACAGAGCA 2392

Qy 749 GTCAACATCGCCAAAGCAGGGCAAACTGCCCGCTCTAGCTCACCAGGTTGATGAGCAAGGG 808

Db 2393 GTCAACATCGCCAAAGCAGGGCAAACTGCCCGCTCTAGCTCACCAGGTTGATGAGCAAGGG 2452

Qy 809 GCGGCCGAGCCATCGCTCAGGCCAAGCGCAGAGGGTGTCTGTTTGGGGAGCCCATC 868

Db 2453 GCAGCTGACATGTTGCTCCCAAGCGCAGGGGGTGTCTGCTTTTGGGGAACTATC 2512

Qy 869 ACCGCCAGCTGGGCGACCGACGCTTCACTACTGAGGAGCAAGAACTGGGGCCAGAGCTGCA 928

Db 2513 ACTGCCAGCTGGGCGACCTGATGCTCTCAGCTACTTGGAGCAAGAACTGGGGCCAGAGCTGCA 2572

Qy 929 GCCTTCGTCACTACACCCCTGTCAACCCAGACCCCAACCGGACCTTACTTCTGACGACCACTC 988

Db 2573 GCCTTCGTCACTTCAACCCCTTATCAACCCGACCTTACTTCTGACGACCACTC 2632

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Db 2693 CAGAGGCTGTGGGCAAGGACAACTTTCGGCTGATCCCGAGGGGAGTCAACCGTATAGAA 2752

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Db 2753 GAGCGCATGTCTGTGTCTGGGAGAAATGTGGCTCTTGGGAGAAATGAGAGAGATGAG 2812

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Qy 1349 CGGGAGCGCTGCGCTGTGTCATAAGTCAAGGCGCGAGTGGCTGGAGGACGGGAGAGATG 1408

Db 2993 CGAGGAGTGCCTCACCGTGTGTCATAAGTCAAGGCGCAGAGTGGTGTGGAGGACGGGAACTG 3052

Qy 1409 TTTGTCAACCCCGGGGGGGGGCTTTCCTCTCGGAAACATTCGGGACTTTGTCTAC 1468

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Qy 1469 AAGAGGATCAAAAGCTCGCAACAGGCTGGGGAGATCACGGTGTGCCCGCTGGGCTGTAT 1528

Db 3113 AAGAGGATCAAAAGCTCGCAACAGGCTAGCAGAGATCAACGGTGTGCTTCGAGGCGCTGTAT 3172

Qy 1529 GACGGGCGCTCCACAGGTTGATGTTGCTTGCACCAAGCAGGGAGTGGCGCTCCGGCCCGC 1588

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Qy 1589 GCGTCTCGCCAGGCAAGATCTCCGCTGCTCTGTTGGGCAACCTATCATGTCGGGGTTC 1648

Db 3233 GCATCTCTGTTTCCAGGCAAGATCTCAGTGTCCACCGCTGCGCAACCTGCACCAAGTGGGGTTC 3292

Qy 1649 AGCCTATCTGGGCTCTCAGGCTGATGACCACTGCGCCGAGC 1689

Db 3293 AGCCTATCTGGCTCTCAGGCTGACGATCAATGTCAGAGC 3333

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RESULT 3
BX353556      1016 bp      mRNA      linear      EST 08-APR-2004
LOCUS        BX353556 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION   cDNA clone CS0DC008YB05 5-PRIME, mRNA sequence.
ACCESSION    BX353556
VERSION      BX353556.2 GI:46290133
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1016)
AUTHORS     Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On May 5, 2003 this sequence version replaced gi:30371778.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5694.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC008AC030P1&c=5694.f.
FEATURES             source
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     /note="1st strand cDNA was primed with a NotI-oligo(dT)
     primer. Five prime end enriched, double-strand cDNA was
     digested with Not I and EcoR V sites of the Not I and EcoR V
     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      54.9%; Score 928.6; DB 5; Length 1016;
Best Local Similarity 96.2%; Pred. No. 8.3e-198;
Matches 982; Conservative 19; Mismatches 14; Indels 6; Gaps 5;

QY 208 CGCCACGGCTGATGGTCTCTCTGGTGGCGTTGAGTCCACACGAAGGCTGCAGATGCC 267
DB 1 CGCCACGGCTGATGGTCTCTCTGGTGGCGTTGAGTCCACACGAAGGCTGCAGATGCC 60

QY 268 TGTCTGGGATGACACCGGCTGACGACTTCTGTTCAGGGGACCAAGGACGGCTAGCAGG 327
DB 61 TGTCTGGGATGACACCGGCTGACGACTTCTGTTCAGGGGACCAAGGACGGCTA-CAGG 119

QY 328 AGGAACACCATGATCTTGACACGCTCTCCCGACACGGGTGTGAGCTGTGGCGGC 387
DB 120 AGGAACACCATGATCTTGACACGCTCTCTCCCGACACGGGTGTGAGCTGTGGCGGC 179

QY 388 CTACGAGCAGTGGCGGAGCGGGCGGACAGCGGGCGCTGTGGGACTACTCCCTGCACGT 447
DB 180 CTACGAGCAGTGGCGGAGCGGGCGGACAGCGGGCGCTGTGGGACTACTCCCTGCACGT 239

QY 448 GGCATCACCGATGGATGAGAGCATCAAGAGGAGCTGGAGGCGCTGTGTCAAGGAGAA 507
DB 240 GGCATCACCGATGGATGAGAGCATCAAGAGGAGCTGGAGGCGCTGTGTCAAGGAGAA 299

QY 508 GGGGTGAATCTCTCTGTCTTCATGGCATCAAGGACCGGTGCCAGTGCAGCGACAG 567
DB 300 GGGGTGAATCTCTCTGTCTTCATGGCATCAAGGACCGGTGCCAGTGCAGCGACAG 359

QY 568 CCAGATGTACGAGATCTTACGATCATCCGGGACCTTGGGGCGCTTGGCCCGAGGTGCACGC 627

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DB 360 CCAGATGTACGAGATCTTTCAGCATCATCCGGACCTCGGGGGCTTGG-CCAGGTGCACGC 418
QY 628 TGAGAACGGGGACATCGTGGAGAGGAGCAGAAAGCGTTGCTGGAGCTCGGCATCACTGG 687
DB 419 TGAGAACGGGGACATCGTGGAGAGGAGCAGAAAGCGTTGCTGGAGCTCGGCATCACTGG 478
QY 688 CCCCAGAGGCGCAGCTGCTCAGCCACCCAGAGAGGTGAGGGCTGAGGCGGTTGACCGAGC 747
DB 479 CCCCAGAGGCGCAGCTGCTCAGCCACCCAGAGAGGTGAGGGCTGAGGCGGTTGACCGAGC 538
QY 748 TGTACACATCGCCAAAGCAGGCAAACTGCCCCCTGTACCTGTCACCAAGGTGATGAGCAAGGG 807
DB 539 TGTACACATCGCCAAAGCAGGCAAACTGCCCCCTGTACCTGTCACCAAGGTGATGAGCAAGGG 598
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QY 988 CTGCTGCTCAGGCGGGGACCTCAGGTGACAGGCGGCGGCTGACCTTCACTGACCTGC 1047
DB 779 CTGCTGCTCAGGCGGGGACCTCAGGTGACAGGCGGCGGCTGACCTTCACTGACCTGC 838
QY 1048 CCAGAAAGGCTGTGGGCAAGGACAACTTTCGCGCTGATCCCGGAGGCGACCAACGGGCAATTGA 1107
DB 839 CCAGAAAGGCTGTGGGCAAGGACAACTTTCGCGCTGATCCCGGAGGCGACCAACGGGCAATTGA 898
QY 1108 GGAGCGCATGTGAT-GGTCTGGAGAAATGTGTGCGCTCTGGAGAGATGGACGAGAATG 1166
DB 899 GGAGCGCATGTGATGGTCTGGAGAAATGTGTGCGCTCT-KGAARATKGACGARAATD 957
QY 1167 AGTTGCTGCGGTGACCATGACAAATGCTGCGCAAAATCTTCAATTTTACCAGGAAGG 1226
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QY 1227 G 1227
DB 1016 G 1016

RESULT 4
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LOCUS        BX356921
DEFINITION   5', mRNA sequence.
ACCESSION    BX356921
VERSION      BX356921.1 GI:22372399
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 938)
AUTHORS     NIH-MGC http://imgc.nhl.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: The I.M.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2562 row: g column: 16

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FEATURES
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/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match
Best Local Similarity 98.4%; Pred. No. 1.1e-186; Length 938;
Matches 938; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Qy 614 GCCAGGTGACGCTGAGAACGGGACATCGTGAGGAGGAGCAGAAAGCGGTTGCTGGAG 673
Db 1 GGCCAGGTGACGCTGAGAACGGGACATCGTGAGGAGGAGCAGAAAGCGGTTGCTGGAG 60

Qy 674 CTGGCATCATCTGCCCGGAGGCGACGTCTCAGCCACCCCGAGGAGGTGGAGCTGAG 733
Db 61 CTGGCATCATCTGGCCCGGAGGCGACGTCTCAGCCACCCCGAGGAGGTGGAGCTGAG 120

Qy 734 GCGGTGTACCGAGCTGTCAACATCGCCAAAGCAGGCAAACTGCCCGCTGTACGTCAACAA 793
Db 121 GCGGTGTACCGAGCTGTCAACATCGCCAAAGCAGGCAAACTGCCCGCTGTACGTCAACAA 180

Qy 794 GTGATGACGAAGGGGGCGGCGACGCATCGCTCAGCCCAAGCGCAGAGGGGTGGTCGTG 853
Db 181 GTGATGACGAAGGGGGCGGCGACGCATCGCTCAGCCCAAGCGCAGAGGGGTGGTCGTG 240

Qy 854 TTTGGGAGGCCATCAGCGCGAGCTGGCCACCGACGGTTCACTACTGAGCAAGAAC 913
Db 241 TTTGGGAGGCCATCAGCGCGAGCTGGCCACCGACGGTTCACTACTGAGCAAGAAC 300

Qy 914 TGGGCCAAGGCTGCAGGCTTGTGTCAATCAATCAATCAATCAATCAATCAATCAATCA 973
Db 301 TGGGCCAAGGCTGCAGGCTTGTGTCAATCAATCAATCAATCAATCAATCAATCAATCA 360

Qy 974 GACCACCTCACTGCTTGTGTTCAGCGGGGACCTCCAGGTGACAGGCGAGCGCCACTGC 1033
Db 361 GACCACCTCACTGCTTGTGTTCAGCGGGGACCTCCAGGTGACAGGCGAGCGCCACTGC 420

Qy 1034 ACCTTACCACTGCGCCAGAGGCTGTGGCAGAGCAAACTTCGCGCTGATCCCGAGGCG 1093
Db 421 ACCTTACCACTGCGCCAGAGGCTGTGGCAGAGCAAACTTCGCGCTGATCCCGAGGCG 480

Qy 1094 ACCAAGGCGATGAGGAGCGCATGTGCTGTGGGAGAAATGTGTGGCTCTGGGAAG 1153
Db 481 ACCAAGGCGATGAGGAGCGCATGTGCTGTGGGAGAAATGTGTGGCTCTGGGAAG 540

Qy 1154 ATGACGAGAAATGAGTTTGTGTGCGGCTGACCAAGTACCAATGTGCAAAATCTTCAATTT 1213
Db 541 ATGACGAGAAATGAGTTTGTGTGCGGCTGACCAAGTACCAATGTGCAAAATCTTCAATTT 600

Qy 1214 TACCAAGGAGGGCGAGTGGCTGTGGCTGTGACGCTGACCTGTGATATGAGACCCC 1273
Db 601 TACCAAGGAGGGCGAGTGGCTGTGGCTGTGACGCTGTGATATGAGACCCC 660

Qy 1274 AAGGCCACCAAGATCATCTCTGCCAAGACCCCAATCTGAACGTGGAGTACACATCTTC 1333
Db 661 AAGGCCACCAAGATCATCTCTGCCAAGACCCCAATCTGAACGTGGAGTACACATCTTC 720

Qy 1334 GAGGAGTGGAGTCCGGGAGGCGCTGCCGTGTCATTAAGTCAGGGCCAGTGGCGCTG 1393
Db 721 NNAGGAGTGGAGTCCGGGAGGCGCTGCCGTGTCATTAAGTCAGGGCCAGTGGCGCTG 780

Qy 1394 GAGGACGGGAAGATGTTTGTCA-CCCGGGGGGGCGGCTTCGT-CCCTCGGAACACAT 1451
Db 781 GAGGACGGGAAGATGTTTGTCA-CCCGGGGGGGCGGCTTCGT-CCCTCGGAACACAT 840

Qy 1452 TCCCGGACTTGTCTCAAGAGGATCAAAAGCTCGCAACAGGCTGGCGGAGATCCACGGTG 1511
Db 841 TCCCGGACTTGTCTCAAGAGGATCCAAAGCTCGCAACAGGCTGGCGGAGATCCACGGTG 900

Qy 1512 TG-CCCGGTGGCTGTATGACGGGCGGCTTCAC 1543
Db 901 TGCCCGGTGGCTGTATGACGGGCGGCTTCAC 933

RESULT 5
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LOCUS AGENCOURT 6699737 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5769897
DEFINITION 5', mRNA sequence.
ACCESSION BM927995
VERSION BM927995.1 GI:19378374
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1075)
NIH-MGC http://mgi.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12832 row: b column: 10
High quality sequence stop: 634.
FEATURES
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/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 51.6%; Score 872.6; DB 5; Length 1075;
Best Local Similarity 96.1%; Pred. No. 3.2e-185;
Matches 938; Conservative 0; Mismatches 30; Indels 8; Gaps 4;

Qy 1 GCGGCGCCCTTACAGAGACCCCGAGGAGCAGGATGCTTCCAGGCGCAAGAAAGCATCCC 60
Db 2 GCGGCGCCCTTACAGAGACCCCGAGGAGCAGGATGCTTCCAGGCGCAAGAAAGCATCCC 61

Qy 61 CCGGATCAAGAGTACCGGCTTCTTGATCAGAGGTGGGAGGATCGTGAATGACGACCATC 120
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Db	62	CCGATACGAGTGACCGGCTTCTGATCAGAGTGGAGGATCGTGAATGACGACCGCAGTC	121
Qy	121	CTTTTACGCTGATGTGCACTGGAAGATGCTTGTATATAAACAATCGGAGAAACCTCAT	180
Db	122	CTTTTACGCTGATGTGCACTGGAAGATGCTTGTATATAAACAATCGGAGAAACCTCAT	181
Qy	181	CGTCCCTGGGGGATCAAGACCAATTCAGCCCAAGCCCTGATGGTCTTCTTGGTGGCGT	240
Db	182	CGTCCCTGGGGGATCAAGACCAATTCAGCCCAAGCCCTGATGGTCTTCTTGGTGGCGT	241
Qy	241	TGACGTCCACACAGGCTGCAGATGCTGTCTGGGCATGACACCGGCTGACGACTTCTG	300
Db	242	TGACGTCCACACAGGCTGCAGATGCTGTCTGGGCATGACACCGGCTGACGACTTCTG	301
Qy	301	TCAGGGCACCAAGGACGCTAGCAGAGGAACCAACATGATCTTGGACCACTCTTCCC	360
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Qy	361	CGACACGGGTGTGAGCTGTCTGGGCTTACGAGCAGTGGCGGAGCGGCGACAGCGC	420
Db	362	CGACACGGGTGTGAGCTGTCTGGGCTTACGAGCAGTGGCGGAGCGGCGACAGCGC	421
Qy	421	GGCTCTGCTGCACTACTCCCTGCACGTGGACATCACCCGATGGCATGAGCATCAAGGA	480
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Qy	481	GGAGCTGGAGGCCCTGTCTAGAGAGAGGGTGTGAATCTCTTCTGTCTTATGGCAT	540
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Db	602	CTTGGGGGCTTGGCCCAAGTGCACGTGAGAACGGGACATCTGTGAGGAGGAGCAGAA	661
Qy	661	GCGGTGTGAGCTGGCATCTGCCCCGAGGCGACGTGCTCAGCCACCCGAGGA	720
Db	662	GCGGTGTGAGCTGGCATCTGCCCCGAGGCGACGTGCTCAGCCACCCGAGGA	721
Qy	721	GGTGGAGGCTGAGCGGTGTACCGAGCTGTACCATCGCCCAAGCAGCAGCACTGCCGCT	780
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Qy	781	GTACGTCAACCAAGGTGATGAGCAAGGGGGCGCGCGCATCGCTCAGGCCAAGCGCAG	840
Db	782	GTACGTCAACCAAGGTGATGAGCAAGGGGGCGCGCGCATCGCTCAGGCCAAGCGCAG	841
Qy	841	A--GGGGTGTCTGTTTGGGAGCCCATCAGCCAGCGCT--GGGACCGAGCGGTTTACA	897
Db	842	AAGGGTGTCTGTTTGGGAGCCCATCAGCCAGCGCT--GGGACCGAGCGGTTTACA	901
Qy	898	CTACTGGAGCAAGCACTGGGCCAA--GGCTGAGCTTCTGTCACATCA--CCCCCTGTC	952
Db	902	CTACTGGAGCAAGCACTGGGCCAAAGGGCCGCGAGCCCTTCTGCCATTACCCCTGTTTC	961
Qy	953	AACCCAGACCCCAACCA 968	
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RESULT 6			
AK077000			
LOCUS			
DEFINITION			
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931422N23 product:dihydropyrimidinase-like 3, full insert sequence.			
AK077000			
ACCESSION			
VERSION			
KEYWORDS			

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayata, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
MEDLINE	
PUBMED	
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	
PUBMED	
REFERENCE	6 (bases 1 to 1899)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Niehi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, F., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://phantom.gsc.riken.jp/ Location/Qualifiers
FEATURES	1. .1899
SOURCE	

[illegible]

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5694.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CSODF015CD100P1&c=5694.f.

FEATURES

source

Location/Qualifiers
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 /tissue_type="PETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens PETAL BRAIN"
 /notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 48.7%; Score 823.2; DB 5; Length 857;
 Best Local Similarity 99.4%; Pred. No. 3.9e-174;
 Matches 855; Conservative 2; Mismatches 0; Indels 3; Gaps 3;
 QY 5 CCCTACACAGAGCCCCCAGGACGAGATGCTTCAGGGGCAAGAAAGCATCCCCCG 64
 DB 1 CCCCTACACAGAGCCCCCAGGACGAGATGCTTCAGGGGCAAGAAAGCATCCCCCG 60
 QY 65 ATCAGAGTGACCGCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACCACTCTTT 124
 DB 61 ATCAGAGTGACCGCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACCACTCTTT 120
 QY 125 TAGCTGATGTGACGTGGAAGATGCTTGATATAAAACAAATCGAGAAACCTTCATCGTC 184
 DB 121 TAGCTGATGTGACGTGGAAGATGCTTGATATAAAACAAATCGAGAAACCTTCATCGTC 180
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 QY 485 CTGGAGGCGCTGTCAAGGAGAGGGTGTGAATCTCTTCTGTTTCATGGCATCAAG 544
 DB 480 CTGGAGGCGCTGTCAAGGAGAGGGTGTGAATCTCTTCTGTTTCATGGCATCAAG 539
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 DB 540 GACCGTGTCCAGTGCAGCAGCAGCATGATAGAGATCTTCAGCATCATCCGGGACCTG 599
 QY 605 GGGGCTTGGCCCCAGGTGCACGCTGAGAACCGGGAATCTGTTGGAGGAGGACAGAGCGG 664

Db 600 GGCGCTTGG-CCAGGTGCACGCTCAGAACGGGACATGTRGAGGAGGAGCAGAGCGG 658
 QY 665 TTGCTGGAGCTCGGATCATCTGCCCCCGAGGGCCAGTGCTCAGCCACCCCGAGGAGGTG 724
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 Db 718 GAGGCTGAGGCGGTGTACCGAGCTGTCAACATGCGCCAGCAGGCAACCTGCCGCTGTAC 777
 QY 785 GTCAACCAAGGTGATGAGCAAGGGCGGCGCCAGCGCATCGCTCAGGCCAAGCGCAGAGG 844
 Db 778 GTCAACCAAGGTGATGAGCAAGGGCGGCGCCAGCGCATCGCTCAGGCCAAGCGCAGAGG 837
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 Db 838 GTGCTGCTGTTTGGGAGCC 857
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 AK090197
 LOCUS
 DEFINITION
 Mus musculus 11 days embryo spinal cord cDNA, RIKEN full-length
 enriched library, clone:G630016E18 product: dihydropyrimidinase-like
 4, full insert sequence.
 ACCESSION
 AK090197
 VERSION
 AK090197.1 GI:26105790
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
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http://www.genoscope.cns.fr/cdna?s=CS0DB005CC06QP1&c=5694.f.
FEATURES
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        /notes="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
  Query Match      47.6%; Score 804.6; DB 5; Length 963;
  Best Local Similarity 99.4%; Pred. No. 6e-170;
  Matches 848; Conservative 1; Mismatches 0; Indels 4; Gaps 4;

QY 12 CAGAGACCCCGAGGAGGATGCTCTCCAGGGCAAGAAACATCCCCCGGATCACGA 71
DB 1 CAGAGACCCCGAGGAGGATGCTCTCCAGGGCAAGAAACATCCCCCGGATCACGA 60

QY 72 GTGACCGCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCATGCTCTTTACGCTG 131
DB 61 GTGACCGCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCATGCTCTTTACGCTG 120

QY 132 ATGTGCACTGGGAAGATGGCTTGATAAAAAATAATCGGAGAAACCTCATGCTCCCTGGGG 191
DB 121 ATGTGCACTGGGAAGATGGCTTGATAAAAAATAATCGGAGAAACCTCATGCTCCCTGGGG 180

QY 192 GCATCAAGACCATGACGGCCACCGCTGATGTGCTCTTCTGTGGGTGAGTGCATCACCA 251
DB 181 GCATCAAGACCATGACGGCCACCGCTGATGTGCTCTTCTGTGGGTGAGTGCATCACCA 240

QY 252 CAAGGCTGCAGATGCTCTGCGGATGACACCGCTGACGACTTCTGTGACGGGACCA 311
DB 241 CAAGGCTGCAGATGCTCTGCGGATGACACCGCTGACGACTTCTGTGACGGGACCA 300

QY 312 AGGACGCTAGCAGGAGGAACACCATGATCTTTGGACACGCTCTTCCCGACACGGGTG 371
DB 301 AGGACGCTA-CAGGAGGAACACCATGATCTTTGGACACGCTCTTCCCGACACGGGTG 359

QY 372 TGAGCTGTGCGGGCTTACGACAGTGGCGGAGCGGGGAGACAGCGCGGCTGTGCTGG 431
DB 360 TGAGCTGTGCGGGCTTACGACAGTGGCGGAGCGGGGAGACAGCGCGGCTGTGCTGG 419

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QY 612 TGGCCAGGCTGACGCTGAGAACGGGACATCGTGGAGGAGGAGCAGAGCGGTTCGCTGG 671
DB 599 TGG-CCAGGTGCACGCTGAGAACGGGACATCGTGGAGGAGGAGCAGAGCGGTTCGCTGG 657

QY 672 AGCTCGGCATCACTGGCCCCGAGGGCCACGCTGTCTAGCCACCCCGAGGAGGTGAGGCTG 731
DB 658 AGCTCGGCATCACTGGCCCCGAGGG-CACGTGTCTAGCCACCCCGAGGAGGTGAGGCTG 716

QY 732 AGCGGTGTACCGAGCTGTACCATGCGCAGCAGGCAAACTGCCCGCTGTAGTCAACCA 791
DB 717 AGCGGTGTACCGAGCTGTACCATGCGCAGCAGGCAAACTGCCCGCTGTAGTCAACCA 776
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792 AGGTGATGAGCAAGGGGGGGCGCGCATCGCTCAGGCCAAGCGAGGGGTGGTGG 851
777 AGGTGATGAGCAAGGGGGGGCGCGCATCGCTCAGGCCAAGCGAGGGGTGGTGG 836
852 TGTGTTGGGAGCC 864
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RESULT 10
BM928281
LOCUS
DEFINITION
  AGENCOURT 6699776 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770115
  5', mRNA sequence.
ACCESSION
  BM928281
VERSION
  BM928281.1 GI:19378660
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1105)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-r@mail.nih.gov
  Tissue Procurement: Life Technologies, Inc.
  cDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM12832 row: k column: 12
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      Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
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      and male age 26 weeks. Library is oligo-dT primed and
      directionally cloned (EcoRV site is destroyed upon
      cloning). Average insert size 1.7 kb, insert size range
      0.7-3.5 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (Invitrogen). Research Genetics tracking code 017. Note:
      this is a NIH_MGC Library."
ORIGIN
  Query Match      47.1%; Score 795.8; DB 5; Length 1105;
  Best Local Similarity 93.9%; Pred. No. 5.8e-168;
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QY 181 CGTCCCTGGGGGCATCAAGACCATTGACGCCCAAGGCTGATGCTTCTTGGTGGCGT 240
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QY 241 TGACGTCCACACAAAGGCTGCAGATGCTCTCTTGGGCATGACACCGGCTTGACGACTTCTG 300
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241 Db TCAGGGCAACCAAGGCAAGGCTAGCAGGAGGAAACACCATGATCTTGGACCAAGCTTCTCC 300
361 Qy CGACACGGGTGTGAGCTGCTGGCGGCTACGAGCAAGTGTGGCGGAGCGGCGGACAGCGC 420
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421 Qy GGCTGTGCTGAGCTACTCCCTGCAAGGAGGAGGAGTGTGAACTCTCTTCTGCTTTCATGGGATA 540
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661 Qy GCGGTGCTGAGCTCGGCTACCTGCGCCCGAGGCGCCAGTGTCTCAGCCACCGCGAGGA 720
Db GCGGTGCTGAGCTCGGCTACCTGCGCCCGAGGCGCCAGTGTCTCAGCCACCGCGAGGA 660
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Db GTAGCTACCAAGGTGATGAGCAAGGGGGCGCCGACGATCTCAGCCCAAGCGCAG 780
841 Qy AGGGTGGTGC---GTGTTTGGGGAGCCCATCCCGCCAGCGCTGGGCAACCGG 892
Db AGGGTGGTGC---GTGTTTGGGGAGCCCATCCCGCCAGCGCTGGGCAACCGG 840
893 Qy TCACACTACTGG--AGCAAGAACTGGGCGCAAGG---CTGCAAGCTTCTGTCACATCAACCC 947
Db CCCCCCTACTGGGAGGCAAGAACTGGGCGCCAGGCCCCCAGGCTTTCGGACCTCAACCC 900
948 Qy C--TGTCACCCAGACCCCAAGCGGAGACCACTTCACTTGT 989
Db CTTTGTCAACCCAAAGCCCGGAGACCCCGGAGACCCCTTCCCTGCT 944

RESULT 11

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LOCUS AGENCOURT_6792381 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5769039
5', mRNA sequence.

ACCESSION BQ68024

VERSION BQ68024.1 GI:19897070

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1058)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LUAM12829 row: n column: 16

High quality sequence stop: 676.

FEATURES

source

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fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 47.0%; Score 795; DB 5; Length 1058;
Best Local Similarity 97.5%; Pred. No. 8.7e-168;
Matches 818; Conservative 0; Mismatches 17; Indels 4; Gaps 1;
Qy 1 GC CGC C C C C T A C C A G A G A C C C C A G G A G C A G A T G C T T C C A G G C G A A G A A A G C A T C C C 60
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Qy 61 C C G G A T C A C G A G T G A C G C C T T C T G A T C A G A G T G G A G A T C G T G A A T G A C G A C C A G T C 120
Db 129 C C G G A T C A C G A G T G A C G C C T T C T G A T C A G A G T G G A G A T C G T G A A T G A C G A C C A G T C 188
Qy 121 C T T T T A C G T G A T G C A C G T G G A A G T G C T T G A T A A A A C A A T C G G A G A A A C C T C A T 180
Db 189 C T T T T A C G C T G A T G T G C A G T G A A G A T G C T T G A T A A A A C A A T C G G A G A A A C C T C A T 248
Qy 181 C G T C C C T G G G G G C A T C A A G A C C A T T G A C C C C A C G C C T G A T G T C C T C T G T G C G C T 240
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Qy 241 T G A C G T C C A C A A A G C T G C A G A T G C T G T C T T G G G C A T G A C A C C G C T G A C G A C T T C T G 300
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Qy 421 G G C T G C T G C G A C T A C T C C C T G C A C G T G G A C A T C A C C C G A T G C A T G A G A G A T C A A G G A 480
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

This sequence belongs to sequence cluster 5694.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DF028CF05Q0P1&c=5694.f>.

FEATURES

source

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/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
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enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

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ORIGIN

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Query Match 46.7%; Score 790; DB 5; Length 1042;
Best Local Similarity 91.0%; Pred. No. 1.2e-166;
Matches 829; Conservative 24; Mismatches 56; Indels 2; Gaps 2;

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DB 173 CCGGATCAGGAGTACCGCTTCTGATCAGAGTGGGAGGATCGTGAATCAGCAGTC 232
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QY 181 CGTCCCTGGGGGATCAAGACCATGACCGCTGATGCTGATGCTCTTCGTTGGTGGCT 240
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QY 241 TGAGTCCACAAAGGCTGAGATGCTGCTGCTGGGATGACACCGCTGACGACTTCTG 300
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QY 301 TCAGGGCACCAGGCGCTAGCAGGAGGAACCAACCATGATCTTGACCAACGCTCTTCCC 360
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QY 361 CGACACGGGTGAGCTCTGCGGGCTACGAGAGTGGGGAGCGGGCGGACAGCGC 420
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DB 1012 AMTKGCGMAAG 1022

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RESULT 14

BX444582

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On May 15, 2003 this sequence version replaced gi:30784243.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 5694.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?s=CS0DN004AF01Q0P1&c=5694.f>.

Location/Qualifiers

1. 900

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/mol_type="mRNA"

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/clone="CS0DN004YK01"

/tissue_type="ADULT BRAIN"

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/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Query Match 45.9%; Score 775.4; DB 5; Length 900;

Best Local Similarity 98.3%; Pred. No. 2.2e-163;

Matches 794; Conservative 9; Mismatches 3; Indels 2; Gaps 2;

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QY 241 TGACGTCCACACAAAGCTGCAGATGCTGTCTTGGGCATGACACCGCTGACGACTTCG 300
Db 335 TGACGTCCACACAAAGCTGCAGATGCTGTCTTGGGCATGACACCGCTGACGACTTCG 394
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DEFINITION Mus musculus CRMP1 gene, 1680 bp DNA linear GSS 17-DEC-2003
Genomic survey sequence.
ACCESSION AY419150
VERSION AY419150.1 GI:39775110
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1680)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
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JOURNAL PUMED 14671302
REFERENCE 2 (bases 1 to 1680)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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Matches 1028; Conservative 0; Mismatches 591; Indels 0; Gaps 0;
QY 71 AGTGACCGCTTCTGATCAGAGTGGAGGATCGTGAATGACGACGAGTCCTTTACGCT 130
Db 1 AGTGACCGCTTCTCATCAGAGGTGGACGCATCATCAATGATGACGAGTCCTTACGCC 60
QY 131 GATGTGCAGCTGGAAGATGGCTTTGATAAAACAAATCGAGAGAAACCTCATCGTCCCTGGG 190
Db 61 GATGTCTACTAGAGATGGACTCTATAAAACAAATAGGAGAGAACCTGATTTCTCTGT 120
QY 191 GGCATCAAGACCATTTGACGCCACCGCTGTATGGTCTTCTCTGGTGGCGTTGACGTCAC 250
Db 121 GGAGTGAACACCATCGAGCGGAATGGCGAATGGTCAATTCGCCGTGGCATTGATGTCAAC 180
QY 251 ACAGGCTGCAGATGCTTCTTGGGCATGACACCGCTGACGACTTCTGTGAGGACACC 310
Db 181 ACTTACTTCAGAAAGCCCTCCAGGGCATGACCTCGGCTGATGACTTCTTCAGGGCAGT 240
QY 311 AAGGACGCGCTAGCAGGAGGAACCAATGATCTTTGGACCAAGTCTTCCCGACACAGGT 370
Db 241 AAGCAGCGCTGCGAGGTGGAACCAAGATGATCANNNNNNNNNNNNNNNNNNNNNNN 300
QY 371 GTGAGCTGCTGGCGGCTTACGAGCAGTGGCGGAGCGGGGAGCAGCGCGCTGCTGC 430
Db 301 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360
QY 431 GACTACTCCTGCACGTGGACATCACCCGATGGCATGAGAGCATCAAGGAGAGCTGGAG 490
Db 361 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420
QY 491 GCGCTGCTCAAGGAGAGGGTGTGAACCTCTCTCTGGTCTTCATGCATACAGGACCGG 550
Db 421 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480
QY 551 TGCAGTGCAGCAGCAGCCAGATGTACGAGATCTTTCAGCATCATCCGGGACCTGGGGCC 610
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QY 611 TTGGCCAGGTGCAAGCTGAGAACCGGGACATCGTGGAGGAGGAGCAGAACGGTGTCTG 670
Db 541 GTGATCTTATGTCATGACAGAAATGGAGATTTTGATAGCTCAGGAAACAAACCGATCCTG 600
QY 671 GAGTCGGCATCACTGGGCCCGAGGCGCAGTGTCTCAGCACCCCGAGGAGGTGGAGGCT 730
Db 601 GAGTGGGCATCACGGGTCCCGAGGGTCTATGTCTGAGGAGCAGCCCGAGGAGCTGGAGGC 660
QY 731 GAGGCGGTGTACCGAGCTGTACCAATCGCCAAAGCAGGCAAACTGCCCGCTGTACGTCACC 790
Db 661 GAGGCTGTGTTCCGGCTATTGCCATTGTCAGGCGCGGATCAATTGCCCTGTGTACATCACC 720
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Qy	791	AAGTGTATGAGCAAGGGGGGGCGAGCCATCGCTCAGGCCAAGCGCAGAGGGGTGTC	850
Db	721	AAGGTATGAGCAAGAGTGCAGCGGACATCATCGCACTGGCCAGGAAGGTCTCTTT	780
Qy	851	GTGTTGGGAGCCATCAAGCCAGCGCTGGGACCGACGGTTCACTACTGGAGCAAG	910
Db	781	GTCTTCGGTGAAGCCATAGCGCGCAGCTGGGAAACCGATGGCACCCACTACTGGAGCAAG	840
Qy	911	AACGGGCCAAGGCTGCAGCGCTTGTGCATCACTCCCTGTCAACCCAGACCCACCACG	970
Db	841	AACGGGCCAAGGCGAGCTGATTTGTGACTTCCCTCCCTGAGCCCGACCCACCACT	900
Qy	971	GCAGACCACTCACTCTGCTTGTCTCCAGCGGGACCTCCAGGTGACAGGCGGCCAC	1030
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Qy	1031	TGCACCTTCAACCTGCCAGAGGCTGTGGGCAAGGACAACTTCGGCTGATCCCGAG	1090
Db	961	TGTCCCTACAGTACTGCTCAGAAAGGCTGTGGGCAAGGACAACTTCACTGATCCCTGAG	1020
Qy	1091	GGCACCAACCGCATTTGAGGAGCGCATGTTCGATGCTCTGGGAGAAATGTGTGGCTCTGGG	1150
Db	1021	GGTGTCAATGGTATAGAAAGCGGATGACCGTGTCTGGGACAAAGGAGTGGCTACTGGC	1080
Qy	1151	AAGATGGAAGAGAAATGAGTTGCTCGCGTGAACCAAGTACAAATGCTGCCAAATCTTCAAT	1210
Db	1081	AAGATGGAATGAGAACCAAGTTGTAGCCGTCAACAGCACCAACAGCAGCAAGATCTTCAAC	1140
Qy	1211	TTTTACCAAGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGTTCATATGGAAC	1270
Db	1141	CTGTACCCGAGGAAGGTCGGATCGCTGTGGGCTCCGATGCTGACGTAGTCACTGGGAC	1200
Qy	1271	CCCAAGGCCACCAAGATCATCTCTGCCAAGACCCACAACTCTGAACGTGGAGTACACATC	1330
Db	1201	CCAGATGAAGTGAAGACCAATAACAGCCAAAGCCATAAATCAACTGTGGAGTACAAATC	1260
Qy	1331	TTGAGGGAGTGGAGTGCAGGGAGCGCTCGCTGCTCATAGTCAAGGCCGAGTGGCG	1390
Db	1261	TTTGAGGGCATGGAGTGCACGGCTCCCTCCCTGCTGCTCATCAGTCAAGGCAAGATTGTC	1320
Qy	1391	CTGAGGAGCGGGAAGATGTTGTTCACCCCGGGGGGGGGCGCTTGTGCTCTCGGAAACA	1450
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Db	1381	TTCCAGAGCATCTCTACAGCGGTGTCAGGATCAGAAAGCAAGGTTTTCGGGTTCATAGT	1440
Qy	1511	GTGCCCCGTGGCTGTATGACGGGCCCGCTCCACGAGGTGATGGTGCCTGCCAAGCCAGGG	1570
Db	1441	GTTCACAGGGCATGTACGATGGGCTGTGTACGAGGTGCCAGCTACACCCAAACATGCT	1500
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Db	1561	CTCCACAGTCCAACTTTCAGCTTATCAGGTGTCAGATGATGATGACAAATCCAAAGGC	1619

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 1690
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	965.4	57.1	4403	4	US-09-949-016-5632 Sequence 5632, Ap
2	963.8	57.0	5421	4	US-09-814-915A-66 Sequence 66, Appl
3	956.6	56.6	1719	4	US-09-949-016-199 Sequence 199, App
4	876.8	51.9	2841	4	US-09-949-016-4735 Sequence 4735, Ap
5	875.2	51.8	2842	4	US-09-702-705-1800 Sequence 1800, Ap
6	875.2	51.8	2842	4	US-09-736-457-1800 Sequence 1800, Ap
7	875.2	51.8	2842	4	US-09-671-325-1800 Sequence 1800, Ap
8	850.6	50.3	5032	4	US-09-949-016-4321 Sequence 4321, Ap
9	850.6	50.3	5047	4	US-09-949-016-200 Sequence 200, App
10	521.8	30.9	3331	4	US-09-976-594-131 Sequence 131, App
11	389.2	23.0	1524	4	US-09-252-991A-6970 Sequence 6970, Ap
12	389.2	23.0	1611	4	US-09-352-991A-6924 Sequence 6924, Ap
13	389.2	23.0	1782	4	US-09-352-991A-6769 Sequence 6769, Ap
14	389.2	23.0	1909	4	US-09-949-016-5326 Sequence 5326, Ap
15	363.8	21.5	1488	4	US-09-734-237B-61 Sequence 61, Appl
16	317.6	18.8	2113	4	US-10-114-810-1 Sequence 1, Appli
17	295.4	17.5	1491	4	US-09-734-237B-63 Sequence 63, Appl
18	229.6	13.6	2100	3	US-09-836-992-2 Sequence 2, Appli
19	189.2	11.2	1374	4	US-08-415-658-20 Sequence 20, Appl
20	188	11.1	1632	4	US-09-270-767-1366 Sequence 1366, Ap
21	188	11.1	1632	4	US-09-270-767-16648 Sequence 16648, A
22	130.8	7.7	1383	1	US-08-289-709-2 Sequence 2, Appli
23	130.8	7.7	1383	1	US-08-602-656-2 Sequence 2, Appli
24	130.4	7.7	1380	4	US-09-950-772-3 Sequence 3, Appli
25	130.4	7.7	3343	4	US-09-950-772-3 Sequence 7, Appli
26	116.4	6.9	336	4	US-09-270-767-1866 Sequence 1866, Ap
27	116.4	6.9	336	4	US-09-270-767-17148 Sequence 17148, A

28	112	6.6	601	4	US-09-949-016-22041	Sequence 22041, A	
29	112	6.6	601	4	US-09-949-016-199950	Sequence 199950, A	
30	110.8	6.6	601	4	US-09-949-016-22040	Sequence 22040, A	
31	110.8	6.6	601	4	US-09-949-016-199949	Sequence 199949, A	
32	110.8	6.6	81433	4	US-09-949-016-11941	Sequence 11941, A	
33	110.8	6.6	84227	4	US-09-949-016-17374	Sequence 17374, A	
C	34	109.6	6.5	601	4	US-09-949-016-168120	Sequence 168120, A
35	109.6	6.5	72549	4	US-09-949-016-16477	Sequence 16477, A	
36	106	6.3	601	4	US-09-949-016-22078	Sequence 22078, A	
37	106	6.3	601	4	US-09-949-016-200054	Sequence 200054, A	
38	102.2	6.0	66988	4	US-09-949-016-11942	Sequence 11942, A	
39	102.2	6.0	66989	4	US-09-949-016-16063	Sequence 16063, A	
C	40	96.6	5.7	601	4	US-09-949-016-154109	Sequence 154109, A
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42	91.4	5.4	444	4	US-09-513-999C-8209	Sequence 8209, Ap	
43	87.8	5.2	601	4	US-09-949-016-22077	Sequence 22077, A	
44	87.8	5.2	601	4	US-09-949-016-200053	Sequence 200053, A	
45	81.8	4.8	1377	4	US-09-916-501A-4	Sequence 4, Appli	

ALIGNMENTS

RESULT 1

US-09-949-016-5632
; Sequence 5632, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5632
; LENGTH: 4403
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5632

Query Match 57.1%; Score 965.4; DB 4; Length 4403;
Best Local Similarity 73.6%; Pred. No. 4.1e-215;
Matches 1230; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

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QY	140	GTGGAAGATGGCTTGATAAAACAAATCGGAGAAACCTCATCGTCCCTGGGGCATCAAG	199
DB	430	ATGGAAGATGGCTTGATCAAGCAAAATAGGAGAAATCTGATTGTGCCAGGAGTGAAG	489
QY	200	ACCATGAGCCCAACCGCTGATGGTCTTCTGTTGGGCTTACGCTCCACACAGGCTG	259
DB	490	ACCATGAGCCCACTCCCGGATGGTGTATCCCGGAGGAATTCACGCTCCACACTCGTTTC	549
QY	260	CAGATGCTGCTGTCGGCATGACACCGCTGACGACTTCTGTGAGGCGACCAAGGACGG	319
DB	550	CAGATGCTGATCAGGGAATGACGCTGCTGATGATTTCTTCCAGGAACCAAGGGGCGC	609
QY	320	CTAGCAGGAGGAACCAACCATGATCTTGGACCACTTCTCCCGACACAGGGGTGTGAGCTG	379

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Db 670 CTGGCTGCCCTTTGACCACTGGAGGGAATGGGCGGACAGCAAGCTCTGCTGTGACTACTCT 729
Qy 440 CTGCACTGTGACATCAACCCGATGGCATGAGAGCATCAAGAGGAGCTGGAGGCGCTGGTC 499
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RESULT 2

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US-09-814-915A-66
; Sequence 66, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relate
; TITLE OF INVENTION: Thereto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 5421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-66
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Query Match 57.0%; Score 963.8; DB 4; Length 5421;
Best Local Similarity 73.5%; Pred. No. 1e-214;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;
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QY 560 AGCGACAGCCAGATGTACGAGATCTTCAAGCATCATCCGGGACCTGGGGCGCTGGGCCAG 619
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QY 620 GTGCACGCTGAGAAAGCGGACATCGTGGAGAGAGAGAGAGCGGTTGCTGGAGCTCGGC 679
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QY 740 TACCGAGCTGTCAACATCGCAAGCAGGCAAACTGCCCGCTGTACGTCAACAAGGTGATG 799
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QY 1280 ACCAAGATCATCTGCGCAAGACCCCAATCTGAAGTGAAGTACAACTCTTCGAGGA 1339
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Db 2705 GGCAACCTGTGATGTCAACGAGGCTGTGAGCGCTTACATTCCTCCGGAAGCGCTTCCCTGAT 2764
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Db 2765 TTTGTCTTACAAGGATCAAGGCAAGGAGGAGGCTGCTGAGCTGAGAGGGGTTCTCGT 2824
QY 1520 GGGCTGTATGACGGGCGCTTCAAGGAGTGTGCTGCTGCCAAGCGGAGTGGCGCT 1579

RESULT 3

US-09-949-016-199
; Sequence 199, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-199

Query Match 56.6%; Score 956.6; DB 4; Length 1719;
Best Local Similarity 73.5%; Pred. No. 3,4e-213;
Matches 1220; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY 32 ATGTCTTCCAGGGCAAGAAAGCATCCCGGATCACGAGTACCGCTTCTGTGATCAGA 91
Db 1 ATGTCTTATCAGGGGAAGAAATATTTCCACGATCACGAGCGATCGTCTTCTGATCAA 60
QY 92 GTTGGAGGATCTGTGATGAGCAGCAGTCTTTTACGCTGATGCGAGTGGAGATGGC 151
Db 61 GGAGGTAAATTTGTTAATGATGACCACTGCTTATGCGACATATACATGGAAGATGGG 120
QY 152 TTGATAAAAAATAATCGAGAAACCTCATCGTCCCTGGGGGCATCAAGACCATTTAGCGCC 211
Db 121 TTGATCAAGCAATAGAGNAATCTGATTTGTCAGAGGAGTGAACATTCGAGGCC 180
QY 212 CACGGCTGATGCTCTTCTGTGGCTTGACGTCCACAAGGCTGAGATGCTGTGTC 271
Db 181 CACTCCGGATGTGATCCCGGAGGAATTTGACGTCCACACTGTTTCCAGATGCTGTAT 240
QY 272 CTGGGATGACACCGGCTGACGACTTCTGTGAGGACCAAGGCGGCTAGCAGGGA 331
Db 241 CAGGGAATGACGCTGCTGTGATGATTTTTCAGGAAGCAAGCGGCTTGGTGGGGA 300
QY 332 ACCACCATGATCTTGACACAGCTTTTCCCGCACAGGCTGTGAGCTGTGGGGCTTAC 391
Db 301 ACCACTATGATCATTTGACCACTGTTTCTGAGCTTGGGCAAGCTTCTGCTGCTTT 360
QY 392 GAGCAGTGGCGGAGCGGGCGGACAGCGGGCTGTGTGAGCTATCTCCCTGCAAGTGGAC 451
Db 361 GACCACTGGAGGAATGGGCGGACAGCAAGTCTCTGTGTGACTACTCTCTGATGTGAC 420
QY 452 ATCACCGGATGGATGAGAGCATCAAGGAGGAGCTGGAGGCTTGTGCAAGGAGAGGT 511
Db 421 ATCAGCGAGTGGCATAAAGGCGATCCAGGAGGAGATGGAGCGCTTGTGAAGGATCACGG 480

QY 512 GTGAACCTCTTCTGCTCTTCATGGCATACAAGGACCGGTGCGAGTGCAGCGACAGCCAG 571
DB 481 GTAAATCTCTCTGCTGATACATGGCTTTCAAAGATCGCTTCAGCTACCGATTGCCAG 540
QY 572 ATGTAAGAGATCTTCAGCATATCCGGGACCTGGGGCCCTTGGCCCAAGTGCAAGCTGAG 631
DB 541 ATTTATAGAGTACTGAGTGTGATCCGGGATATGGGGCCATAGCCCAAGTCCACGCAGAA 600
QY 632 AACGGGACATCTGTGGAGGAGGACAGAGCGGTGTCTGGAGCTCGGCATCACTGGCCCC 691
DB 601 AATGGCGACATCATTCAGAGGAGGACGACAGAGATCTTGATCTGGGCATCACTGGCCCC 660
QY 692 GAGGGCCACGTGTCTCAGCCACCCGAGGAGGTGAGGCTGAGCGGTGTACCCAGCTGTC 751
DB 661 GAGGGACATGTGTGAGCGGACCTGAGGAGGTGAGGCGGAGCGGTGATCTGCGCATC 720
QY 752 ACCATCGCAAGCAGGCAAACTCCCGCTGTATCGTCAACGAAGTGTAGCAAGGGGGG 811
DB 721 ACCATCGCAACCAAGACCAACTGCCCGCTGTATATCAACGAAGTGTAGCAAAAGCTCT 780
QY 812 GCCAGCGCATCTGCTCAGGCGAAGCGCAGAGGGGTGTGTGTTGGGAGCCCATCAC 871
DB 781 GCTGAGGTATCTGCCCGCAGGACAGGAAAGGGAACTGTGTGTATGCGGAGCCCATCACT 840
QY 872 GCCAGCTGGGACCGACCGGTTCACACTACTGAGCAAGAACTGGGCGCAAGGCTGCAGCC 931
DB 841 GCCAGCTGGGACCGGCTCCCATTAATCTGAGCGAGAACTGGGCGCAAGGCTGTGTC 900
QY 932 TTGCTCACATCACCCCTGTCAAACCGAGCCCAACCGGCGACCACTCACTCACTGCTTG 991
DB 901 TTGCTCACCTCCCGACCCCTTGAGCCCTGATCAACCACTCACTCACTCACTCCTTG 960
QY 992 CTGTCAGCGGGACCTCCAGGTGACAGGAGCGCCCACTGCACTTCACTCACTGCGCCAG 1051
DB 961 CTGTCCTGTGGAGACCTCCAGGTGACAGGAGTGGCCATTTGACGCTTTAACTGCGCCAG 1020
QY 1052 AAGGCTGTGGGCAAGCAACTTTCGGCTGATCCCGAGGCGCACCAAGCGCATTTGAGGAG 1111
DB 1021 AAGGCTGTAGGAAAGCAACTTCACTGATTTCCGAGGGGACCAATGGCACTTGAGGAG 1080
QY 1112 CGCATGTGATGTCTGGGAGAAATGTGTGGCTCTTGGGAGATGGAAGAAATGATGTTTC 1171
DB 1081 CGCATGTGCTGATCTGGGAGCAAGGCTGTGTCACTGGGAGATGGAAGAAACCACTTT 1140
QY 1172 GTGCGGTGACAGTACAAATGTGCGCAAAATCTTCAATTTTACCCAGGAGAGGGCGA 1231
DB 1141 GTGCGCTGTGACAGCAACCAATGAGCCAAAGTCTTCAACCTTTTACCCCGGAAAGGCGC 1200
QY 1232 GTGCGCTGTGGGCTCTGACGCTGACCTGTGATATGGAACCCCAAGGCGCACCAAGATCATC 1291
DB 1201 ATTGCTGTGGGATCCGATGCGGACCTGTGTATCTGGGACCCCGACAGCGTTTAAACCATC 1260
QY 1292 TCTGCCAAGACCAACATCTGAACGTGGAGTACAAATCTTTCGAGGGAGTGGAGTCCGG 1351
DB 1261 TCTGCCAAGACACAAACAGCTCTCTCGATGACAAATCTTTCGAGGATGGAGTCCGC 1320
QY 1352 GGAAGCGCTCCCTGTGATTAAGTACAGGCGCGAGTGGCGCTGGAGGACGGGAGATGTTT 1411
DB 1321 GGCCTCCCACTGTGTGTCTCATCAGCAGGGGAGATTTGCTCTGGAGGACGGCACCCCTGCAT 1380
QY 1412 GTCAACCCCGGGGCGGCGCTTCTGCTCCCGGAAACATTTCCCGGACTTTGTCTACAAG 1471
DB 1381 GTCAACGAGGCTGTGAACGCTTACATTTCCCGGAGCGCTTCTCTGATTTGTGTACAG 1440
QY 1472 AGGATCAAAGCTCGCAACAGGCTGGCGGAGATCCAAGGTGTGCCCGCTGGGCTGTATGAC 1531
DB 1441 CGTATCAAAGCAAGGACAGCTGGCTGAGCTGAGAGGGGTTCCTGTGCGCTGTATGAC 1500
QY 1532 GGGCCGCTCAAGAGTGTGTGCTGCAAGCGGAGTGGCGCTCGGGCCCGCGG 1591
DB 1501 GGAACCTGTGTGAAGTGTGTGAGCGCCCAAGACAGTCACTCCAGGCTCTCTCGGCAAG 1560
QY 1592 TCCTGCGCAGGCAAGATCTCCGTGCTCTCTGTGCGCAACCTATCATCAGTGGGGTTTCAGC 1651

DB 1561 ACCTCTCTGCAAGCAGCAGGCCCCACCTGTCCGGAACCTGCACAGTCTGGATTCACT 1620
QY 1652 CTATCTGGGTCTCAGGCTGATGACACCATCGGCCCGCAGCG 1690
DB 1621 TTGTCTGGTCTCAGATTGATGACAACTTCCCGCCCGC 1659

RESULT 4

US-09-949-016-4735
; Sequence 4735, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 4735
; LENGTH: 2841
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4735

Query Match 51.9%; Score 876.8; DB 4; Length 2841;
Best Local Similarity 70.0%; Pred. No. 1.6e-194;
Matches 1181; Conservative 0; Mismatches 507; Indels 0; Gaps 0;

QY 3 CGCCCTTACAGACCCCGAGCAGGATGTCTTCAGGGCAAGAAAGCATCCCC 62
DB 122 CGCCCGGCGAGGCGCGAGGGGCGCATGTGTACAGGGCAAGAGCATCCCC 181
QY 63 GATACAGAGTGACCGCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACCTTCT 122
DB 182 ACATCAGAGTGACCGACTCTCTCATCAAGGTGACGATCATCAACGATGACCAATCC 241
QY 123 TTTCCTGATGTGACGTGGAAGATGGCTTGATATAAACAATCGGAGAAACCTCATCG 182
DB 242 TTATGCTGACGTCTACCTGGAGGATGGACTTATCAACAATAGGAGAACTTAATCG 301
QY 183 TCCCTGGGGCATCAAGACCATTTGACGCCACCGCTGATGTCTTCTGGTGGCTTG 242
DB 302 TTCTGTGGAGTGAAGACCATTTGAAGCCACCGGCGGATGGTTATTCGCGAGGTATTG 361
QY 243 AGCTCCACCAAGGCTGACAGTCCCTGTCTCTGGGCATGACACCGCTGACGACTTCTGTC 302
DB 362 ATGTCAACAGTACCTGCGAGAGCCCTCCAGGGGATGACTGCGGTGATGACTTCTTCC 421
QY 303 AGGGCAACCAAGGCGCTGACAGGAGGAAACCAACATGATCTTTGGACCAAGTCTTCCCG 362
DB 422 AAGGACCAAGGGCGGCACTGTGGGCGGACCAACGATGATCATTTGACCATTTGTCTCTG 481
QY 363 ACAGGCTGTGAGCTGTGGCGCTTACGAGCGTGGGAGCGGCGGAGCGGCGG 422
DB 482 AACCTGGGTCCAGCTTACTGACCTCTTTCGAGAGTGGGACGAGCAGCTGACACCAAT 541
QY 423 CTGCTGCGACTACTCTCCCTGCACTGAGCATCAACCGATGGCATGAGAGCATCAAGAGG 482
DB 542 CTTGCTGTGATTACTCTCCCTCCAGCTGCAATCAACAGCTGGTACGATGGCTTCGGAGG 601
QY 483 AGCTGAGGCGCTGTGTCAGGAGAGGCTGTGAACTCTTCTCTGCTTCTCATGCGCATACA 542
DB 602 AGCTGAGGCTGTGTCAGGACCAAGGCGTCAATCTTCTTCCAAAGTCTATCATGCGCTATA 661


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Db 602 AGCTGGAGGTGCTGGTGCAGGACAAAGGCGCTCAATTCTCCCAAGTCTACATGCGCCTATA 661
Qy 543 AGGACCGGTCCAGTGCAGGACAGCCAGATGTACGAGATCTTCAGCATATCCGGGACC 602
Db 662 AGGATGTCTACCAAAATGTCGACAGCCAGCTCTATGAAGCCTTTACCTCTTTAAGGGCC 721
Qy 603 TGGGGGCTTTGGCCAGGTCACGCTGAGAACGGGACATCGTGGAGGAGGACAGAAAGC 662
Db 722 TGGAGGCTGTGATCTTGGTCCATGCGAGAAATGGAGATTTGATAGCTCAGGAACAAAGC 781
Qy 663 GGTTCGTGGAGCTCGGACATCACTGGCCCCGAGCCGACCGCTGCTGAGCCACCCCGAGAGG 722
Db 782 GATCTCTGAGATGAGGACATCAAGGCTCCCGAGGACATGCTCCCTGAGCAGACCTGAAGAGC 841
Qy 723 TGGAGGCTGAGGCGGTGTACCGAGCTGTACCAATCGCAAGCAGGACCAACTGCGCCGTGT 782
Db 842 TGGAGGCGGAGGCGGTGTCCGGGCCATCAACCAATGCGGCCGAGTCAACTGCGCCGTGT 901
Qy 783 ACCTCACCAAGGTGATGAGCAAGGGGCGGCCGACGCTCGCTCAGGCCCAAGCGCAGAG 842
Db 902 ACATCACCAAGGTCTAGGCAAGGTGACGCGCCGACATCATGCTCTGGCCGAGAAAG 961
Qy 843 GGTGTGTGTTTTGGGAGCCCATCAACCGCCAGCCTGGGACACGAGCGTTTCACACTACT 902
Db 962 GGGCCCTAGTTTTGGAGAGCCCATTTGCCGACAGCCTGGGGACCGATGGCACCCATTACT 1021
Qy 903 GGAGCAAGACTGGCCCAAGGCTGACGCTTGTGCTCCAGCGGGGACCTCCAGGTGACAGGCA 1022
Db 1022 GGAGCAAGAACTGGCCCAAGGCTGCGGCGGTTCGTGACTTCCCTCCCTGAGCCCGGACC 1081
Qy 963 CCACCAAGGACAGACCACTCACTGCTGTGCTGCTCCAGCGGGGACCTCCAGGTGACAGGCA 1022
Db 1082 CTACCAAGCGGACTACTTGTGACTTCTCTACTTGGGCTGTGGGACTTCAGGTGACAGGCA 1141
Qy 1023 GCGCCCATCTGCACTTCCACCACTGCGCCAGAAAGCTGTGGGCAAGGACAACTTCGCGCTGA 1082
Db 1142 GCGGCCACTGTCCCTACAGCACTGCCCAAGGCGGTGGGCAAGGACAACTTTACCCCTGA 1201
Qy 1083 TCCCGAGGACCAACCGGCAATTTGGAGGCGCATGTGATGCTCGGAGAAATGTGTGG 1142
Db 1202 TCCCGAGGCGTGTCAACGGGATAGAGGCGGATGACCGCTGCTGGGACAAAGGCGGTGG 1261
Qy 1143 CCTCTGGAAAGATGGACGAAATGAGTTCTGTCGGGTGACAGTACAAATGCTGCCAAAA 1202
Db 1262 CTACTGGCAAAATGGATGAGAACAGTTTCTGCTGTCTACAGCAACCAATGAGCCNAGA 1321
Qy 1203 TCTTCAATTTTTTACCAAGGAAGGGCGAGTGTGCTGTGGCTCTGACGCTGACCTGTGCA 1262
Db 1322 TCTTTAACTGTATCCCAAGGAAGGGCGGATTTGCGTGGGCTCGGATGCCGACGTGTGCA 1381
Qy 1263 TATGGAAACCCCAAGGCCACCAAGATCATCTGCGCAAGACCCCAATCTGAAAGTGGAGT 1322
Db 1382 TCTGGGACCCCGCAAGGTTTGAAGACCAATAACAGCCAAAGTCAACAAGTCCGGGTGGAGT 1441
Qy 1323 ACAACATCTTCGAGGAGTGGAGTGCCTGGGAGCGCTGCTGCTGCTATAGTCAAGGCGCC 1382
Db 1442 ACAACATCTTCGAGGAGTGGAGTGCCTGGGAGCGCTGCTGCTGCTATAGTCAAGGCGCC 1501
Qy 1383 GAGTGGCGCTGGAGGACGGGAAGATGTTTGTGTCAACCCGGGGCGGGCGCTTCTGCTCCTC 1442
Db 1502 AGATCGTCTTTGAAGACGGAAACATCAACGCTCAACAGGCGATGGGCGCGCTTCATTCCGC 1561
Qy 1443 GGAACATCTCCGGACTTTGTCTACAGAGGATCAAGCTCGCAACAGGCTGGCGGAGA 1502
Db 1562 GGAAGCGCTTCCCGGAGCACCTGTATACAGCGCTCAAAAATCAAGAAATTAAGGTTTGGAT 1621
Qy 1503 TCCAGGTGTGCCCGTGGGCTGTATGACGGGCGCTGCTCCAGGAGTCAAGTGTGCTGCCA 1562
Db 1622 TGCAAGGGGTTTCCAGGGGCAATGTATGACGGTCTCTGTGTAGGAGTACCACTACACCA 1681
Qy 1563 AGCCAGGAGTGGGCTTCCGGGCGCGGCTGCTGCTGCCAGGCAAGATCTCGCTGCTCCTG 1622
Db 1682 AATATGCAACTCCCGCTCTTTCAGCCAAATCTTTCGCTTCTTAAACACACAGCCGCCCA 1741
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Qy 1623 TGCGCAACTCATCATGCTGGGTTTCAGGCTATCTGGGTTCTCAGGCTGATGACCAATCG 1682
Db 1742 TCAGAAACTCTCACCACTTCAACTTCAGCTTATCAGTCTGCCAGATAGATGACAAATC 1801
Qy 1683 CCCGAGC 1690
Db 1802 CCAGGCGC 1809
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RESULT 6

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US-09-736-457-1800
; Sequence 1800, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1800
; LENGTH: 2842
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1800
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Query Match 51.8%; Score 875.2; DB 4; Length 2842;
Best Local Similarity 69.9%; Pred. No. 3.7e-194;
Matches 1180; Conservative 0; Mismatches 508; Indels 0; Gaps 0;
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Qy 3 CGCCCCCTACAGAGACCCCGAGGACGAGATGCTCTCCAGGGCAAGAAAAGCATCCCC 62
Db 122 CGCCCGGCGAGGGCGCCAGAGGGGCCATGTCTGACAGGCAAGAGAGCATCCGC 181
Qy 63 GGATCAGAGTGAACGCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACAGTCT 122
Db 182 ACATCAGAGTGACCGACTCTCATCAAGGTGGACGGATCATCAACGATGACCAATCCC 241
Qy 123 TTATCGCTGATGTGACGTGGAGATGGCTTGTGATATAAAATCGGAGAAAACCTCATCG 182
Db 242 TTATGCTGACGTCTACCTGGAGGATGGACTTATCAAAACAAATAGGAGAACTTAATCG 301
Qy 183 TCCTCGGGGCAATCAAGACCATTTGACGCCACCGCTGATGGTCTTCTGTTGGGCTTG 242
Db 302 TTCTGCTGGAGTGAAGACCATTTGAAGCCAAACGCGGGAGTGTATTCGCGAGGTATTG 361
Qy 243 AGCTCCACAAAGGCTGACAGATGCTGCTCTGCGCATGACACCGCTGACGACTTCTGTC 302
Db 362 ATGTCAACACGTACTGTGCAAGACCCCTCCAGGGGATGACTGCGGCTGATGACTTCTTCC 421
Qy 303 AGGGCAACGAGCGCTAGCAGGAGAACCAATGATCTTGGACACGCTTCTCCCG 362
Db 422 AAGGGACCAAGGGCGGACCTGGTGGCGGACCAACGATGATCATTTGACCATGTTGTTCTCTG 481
Qy 363 ACACGGGTGTGAGCTGTGCGGCTTAGCAGCAGTGGCGGAGCGGCGGAGCAGCGCG 422
Db 482 AACCTGGTCCAGCTTACTGACCTCTTCGAGAAAGTGGCAAGCAGCTGACACCAAT 541
Qy 423 CTGCTGCGACTTACTCCCTGACGCTGGACATCAACCCGATGGCATGAGAGATCAAGAGG 482
Db 542 CTGCTGTGATTACTCCCTCCACGCTGGACATCAACAGCTGGTACGATGGCGTTTCGGAGG 601
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QY	483	AGCTGGAGGCCCTGGTCAAGGAGAGGGGTGTGAATCTCTTCCTGGTCTTCAATGGCATACA	542
DB	602		
QY	543	AGCTGGAGGGTGGTGGTTCAGGACAAGAGGCGTCAAATTCCTTCCAAGTCTCATGGCCCTATA	661
DB	662		
QY	603	AGGACCGGTGCCAGTGCAGCGACGACGCGCAGATGTACAGAGATCTTCAGCATCATCCGGGACC	602
DB	721	AGGATGTCTACCAATGTCTCGACAGCCAGCTCTATGAAGCTTTTACCTCTCTTAAGGGCC	721
QY	603	TGGGGGCTTTGGCCCAGGTGCAGCTCGAGAACCGGGGACATCGTGGAGGAGGAGCAGAGAAGC	662
DB	722	TGGGAGCTGTGATCTTGGTCCATGCGAANAATGGAGATTTGATAGCTCAGGAAACAAAGC	781
QY	663	GGTGTCTGGAGCTCGGCATCACTGGCCCCGAGGGCCACGTGCTCAGCCAATCCCGAGGAGG	722
DB	782	GGATCTCTGGAGATGGGCATCAGGGTCCGAGGGCCATGCCCCCTGAGCAGACCTGAAAGAGC	841
QY	723	TGAGGCTGAGGGCGGTGTACCGAGCTGTCAACCATCGCCAAGCAGGCAAACTGCCCCGCTGT	782
DB	842	TGAGGGCCGAGGGCGGTGTTCCGGGCCATCAACCAATGCGGGCCGATCAACTGCTGCTGTGT	901
QY	783	ACGTCAACCAAGGTGATGAGCAAGGGGCGCCGACGCGCATCTGCTCAGGCCAAGCGCAGAG	842
DB	902	ACATCAACAAGGTCACTGAGCAAGGTGCGCGGACATCATCGTCTCTGGCCAGAGAAAG	961
QY	843	GGGTGCTGTGTTTGGGGAGCCCATCAACCGCCAGCCTGGGCAACCGACGGTTCACTACT	902
DB	962	GGCCCCTAGTTTTTGGAGAGCCCATTTGCCCGCAGCCTGGGCGACCGATGGCACCATTTACT	1021
QY	903	GGAGCAAGAATCGGCCCAAGGCTGCGAGCTTGTGTCAATCACCCCTGTCTCAACCCAGACC	962
DB	1022	GGAGCAAGAATCGGCCCAAGGCTGCGGCGTTGCTGACTTCCCTCCCTGAGGCCCGGACC	1081
QY	963	CCACCGGCGAGCACACTCACTCCTGTGTGTCCAGCGGGGACCTCCAGGTGACAGGCA	1022
DB	1082	CTACACGCCCGACTACTTGACCTCCCTACTTGGCTGTGGGACTTGCAGGTCAAGGCA	1141
QY	1023	GGGCCACTGTCCCTACAGCACTGCCCAGAAAGCGTGGGCAAGGCAAACTTCGCGCTGA	1082
DB	1142	GGGCCACTGTCCCTACAGCACTGCCCAGAAAGCGTGGGCAAGGCAAACTTTACCCCTGA	1201
QY	1083	TCCCGAGGGCAACCAACGGCATTTAGAGAGCGCATGTGATGGTCTGGGAGAAATGTGTGG	1142
DB	1202	TCCCGAGGGTGTCAACGGGATAGAGAGCGGATGACCGTCTGTGGGCAAGAGCGGTGG	1261
QY	1143	CCTCTGGGAGATGGACGAGATGAGTTCTCGCGGTGACAGGTACAAATGCTGCCAAAA	1202
DB	1262	CTACTGGCAAAATGGATTGAGAACAGTTTGTGCGCTGTCAACAGCACAATTCAGGCCAAGA	1321
QY	1203	TCTTCAATTTTACCCAAGGAAGGGCGAGTGGCTGTGGGCTCTGACGCTGACTCGTGTCA	1262
DB	1322	TCTTTAACCTGTATCCCAAGGAAGGGCGGATTTGCCGTTGGGCTCGGATGCCGAGTGTGTCA	1381
QY	1263	TATGGMAACCCCAAGGCCACCAAGATCATCTCTGCCAAGAGCCCAAAATCTGAAAGTGGAGT	1322
DB	1382	TCTGGGACCCCGACAAGTTGAAGACCATACAGGCCAAAGGTCAAGTCTGCGCGTGGAGT	1441
QY	1323	ACAAATCTTTCGAGGGAGTGAAGTTCGCGGGAGGCGCTGCGGTGTCTAATGTCAGGGCC	1382
DB	1442	ACAAATCTTTCGAGGGTATGGAAGTGCACCGCTCCCCCACTAGTGGTCTATCAGCCAGGGCA	1501
QY	1383	GAGTGGCGCTGGAGGACGGGAGATGTTTGTCAACCGGGGGGGCGGCTGTCCTCCCTC	1442
DB	1502	AGATCTGCTTTTGAAGACGGAAACATCAACGTCAACAAAGGGGATGGGCGGCTTCATTCGGC	1561
QY	1443	GGAAAAATTTCCCGGACTTTTGTCTTACAAGAGGATCAAAAGCTTCGCACACAGGCTGGCGGAGA	1502
DB	1562	GGAAAGGCTTCCGGAGGACCTGTGTACAGCGGTCAAAATCAGGAATAAGGTTTTGGAT	1621
QY	1503	TCCACGCTGTGCCCGTGGGCTGTATGACGGGGCCGCTCCACAGAGGTGATGGTGTCTGCCA	1562
DB	1622	TGCAAGGGGTTTTCAGGGGCGATGATGACGCTCCTGTGTACGAGGTACACAGCTACACCCA	1681

RESULT 7

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RESULT 7
US-09-671-325-1800
; Sequence 1800, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Lique
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1800
; LENGTH: 2842
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1800

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Query Match	51.8%;	Score	875.2;	DB	4;	Length	2842;
Best Local Similarity	69.9%;	Pred. No.	3.7e-194;				
Matches 1180; Conservative	0;	Mismatches	508;	Indels	0;	Gaps	0;

Qy	3	CGCCCCCTACAGAGACCCCCAGAGCAGGATGCTCTTCAGGGCGAAGAAAGCATCCCC	62
Db	122	CGCGCGGGCGAGGGCGCCAGAGGGGGCCATGTCGTACAGGGCAAGAGAGCATCCCG	181
Qy	63	GGATCAGAGTGACCGCTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACAGTCCT	122
Db	182	ACATCAGAGTGACCGACTCTCTCATCAAGGTGGACGGATCATCAACGATGACCAATCCC	241
Qy	123	TTTACGCTGATGTCAGCTGGGAAGATGGCTTGATATAAACAATCGGAGAAAACCTCATCG	182
Db	242	TTTATGTGACGCTTACTGTGGAGTGGACTTATCAAAACAATAGGAGAGACTTAATCG	301
Qy	183	TCCTTGGGGCATCAGACCAATTGACGCCACGGCCTGATGGTCTCTCTGGTGGGGTTG	242
Db	302	TTCTGTGTGGATGTAAGACCAATTGAAGCCAAACGGGGGGATGGTTATTTCCCGSAGGTTTG	361
Qy	243	ACGTCCACACAAGCTGCAGATGCCCTGTCTGTGGGCATGACACCGGCTGACGACTTCTGTC	302
Db	362	ATGTCAACACGTACTGTCAGAGCCCTCCAGGGGATGACTCGGGCTGATGACTTCTTCC	421
Qy	303	AGGGCAACAAGCAGCGCTAGCAGGAGGAACCAACCATGATCTTGGACCAAGTCTTCCCGG	362
Db	422	AAAGGACCAAGGGCGACACTGCTGGCGGGACACAGATGATCATTTGACCATGTTGTCTCG	481
Qy	363	ACACGGGTGTGAGCTGCTGGCGGCCCTTACGAGCAGTGGCGGGAGCGGGCAGACGCGGG	422
Db	482	AACTGGGTCAGGCTTACTGACCTCTTTGAGGAAGTGGCACGAAGCAGCTGACACCAAT	541
Qy	423	CCTGCTGCGACTACTCCCTGACGTGGACATCAACCGATGGCATGAGAGCATCAAGGAGG	482

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Db 542 CCTGCTGTGATTAACCTCCCTCCACGTGGACATCAAGCTGGTACGATGGGTTTCGGGAGG 601
Qy 483 AGCTGAGGCGCCCTGGTCAAGGAGAAAGGTTGTGAATCTCTTCCCTGGTGTTCATGCGCATACA 542
Db 602 AGCTGAGGCTGTGCTGTCAGGACAAAGGCGTCAATTCCTTCCAAAGTCTACATGCGCTATA 651
Qy 543 AGGACCGGTGCTGAGTGCAGGACGACGACGACGATGACGAGATCTTCAGCATCATCCGGGACC 602
Db 662 AGATGTCTACCAAAATGTTCGACAGCCAGCTCTATGAAGCTTTTACCTCTCTTAAGGGCC 721
Qy 603 TGGGGGCTTTGGCCCAAGGTGCACGCTGAGAACGGGACATCGTGGAGGAGGACAGAAAGC 662
Db 722 TGGGAGCTGTGATCTTGGTCCATGACAGAAATGGAGATTTGTAGCTCAGGAACAAAGC 781
Qy 663 GGTGCTGGAGCTCGGATCACTTGGCCCCGAGGGCCACGTGCTCAGGCACCCCGAGGAGG 722
Db 782 GGATCCTGGAGATGGGCATCACGGGTCCCGAGGGCCATGCCCCGTGAGCAGACCTTGAAGAGC 841
Qy 723 TGGAGGCTGAGGCGGTGTACCGAGCTGTACACATCGCAGGAGGCAAACTGCCCGCTGT 782
Db 842 TGGAGGCGGAGCGGTGTTCCGGGCCATCACCAATGGGGCCCGATCAACTGCCCCCTGTGT 901
Qy 783 ACCTCACCAAGGTGATGAGCAAGGGGGCGGCGGACGCTCATGCTCAGGCCCAAGCGCAGAG 842
Db 902 ACATCACCAAGGTGATGAGCAAGGTGACGCGGACGACATCATCGCTCTGGCCAGGAAGAAG 961
Qy 843 GGTGTGTGTTTGGGAGGCCATACACGCGACGCTTGGGACCGGACGAGTGTCACTACT 902
Db 962 GGCCCCCTAGTTTTGGAGAGCCCAATGCGCCAGACCTGGGGACCGGATGGCACCCATTACT 1021
Qy 903 GGAGCAAGAACTGGGCGCAAGCTGCGAGCTTCTGTCATCACCCCCCTGTCAACCCAGACC 962
Db 1022 GGAGCAAGAACTGGGCGCAAGCTGCGGCGTTCGTGACTTCCCCCTCCCTGAGCCCGGACC 1081
Qy 963 CCACCAAGGAGACCACTCACCTGCTTGTGCTCCAGCGGGGACCTCCAGGTGACAGGCA 1022
Db 1082 CTACCAAGCGCGACTACTTGACCTCCCTACTGCGCTGTGGGACTTCAGGTACAGGCA 1141
Qy 1023 GCGCCCACTGCACTTCCACACTGCGCCAGAAAGGCTGTGGGCAAGGACAACTTCGCGCTGA 1082
Db 1142 GCGGCCACTGTCTCCCTACAGCACTGCGCCAGAAAGGCGTGGGCAAGGACAACTTTACCCCTGA 1201
Qy 1083 TCCCGAGGGCACCAAGGATTTGAGGAGCGCATGTCGATGCTCTGGGAAATGTGTGG 1142
Db 1202 TCCCGAGGGGTGCAACGGGATAGAGAGCGGATGACCGCTGCTGTGGGACAGGCGGTGG 1261
Qy 1143 CCTCTGGGAAGATGGAGCGAATGAGTTCTGTCGCGGTGACCAATGCTGCCAAAA 1202
Db 1262 CTACTGGCAAAATGGATGAGAACGAGTTTGTCTGCTGTACCAGCACCAATGCAAGCCAGA 1321
Qy 1203 TCTTCAATTTTACCCAGGAGGGGAGTGGCTGTGGGCTGTAGCGCTGACCTGGTCA 1262
Db 1322 TCTTTAACTGTATCCCAAGGAAAGGGCGGATTCGCTGGGCTCGGATGCGGACGTGTCA 1381
Qy 1263 TATGGAAACCCCAAGGCCACCAAGATCATCTCTGCAAGACCCCAATCTGAAAGTGGAGT 1322
Db 1382 TCTGGGACCCCGACAAGTTGAAGACCAATTAACGCAAAAGTCAAGTTCGGCGGTGGAGT 1441
Qy 1323 ACAACATCTTTCGAGGAGTGGAGTGCCTGGGAGCGCTGCGGTGTCATTAAGTCAGGGCC 1382
Db 1442 ACAACATCTTTCGAGGATGAGGATGAGTGCACCGGCTCCCCACTAGTGGTTCATCAGCCAGGCA 1501
Qy 1383 GAGTGGGCTGTGAGGAGCGGAGAGATGTTTGTGTACCCCGGGGGCGGCGCTTCGTCCCTC 1442
Db 1502 AGATCGCTTTTGAAGACGGAACATCAACGCTCAACAGGGGCATGGGCGCTTCATTCGCG 1561
Qy 1443 GGAATACTTCCCGGACTTTGTCTACAAGAGGATCAAGCTCCGACAGGCTGCGCGAGA 1502
Db 1562 GGAAGGGTTTCCCGAGGACCTGTACAGCGCGTCAAAATCAGGAATTAAGGTTTGTGAT 1621
Qy 1503 TCCACGGTGTGCCCGGTGGCTGTATGACGGGCGCGTCCACGAGGTGATGCTGCTGCCA 1562
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Db 1622 TGCAAGGGGTTTCCAGGGGCATGTATACGGTCTCTGTGTACGAGGTACAGCTACACCCA 1681
Qy 1563 AGCCAGGGAGTGGCGTCCGGCCCGCGCTCTGCCAGGCAAGATCTCGGTGCTCTCTG 1622
Db 1682 AATATGCAACTCCCGCTCTCTTACGCCAAATCTTCGCTTTCTAAACACCGAGCCCCACCCA 1741
Qy 1623 TGGCAACCTACATCATGCTGGGTTTCAGGCTATCTGGGTCCTAGGCTGATGACCAATCG 1682
Db 1742 TCAGAAACCTCCACAGTCCAACTTCAGCTTATCAGTGTCCCGCAGATAGATGACAACATC 1801
Qy 1683 CCGAAGC 1690
Db 1802 CCAGGCGC 1809

RESULT 8
US-09-949-016-4321
; Sequence 4321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4321
; LENGTH: 5032
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4321
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Query Match 50.3%; Score 850.6; DB 4; Length 5032;
Best Local Similarity 70.0%; Pred. No. 2.4e-188;
Matches 1160; Conservative 0; Mismatches 494; Indels 3; Gaps 1;

Qy 18 CCCCCAGGAGCAGGATGCTCTTCCAGGCAAGAAAGCATCCCCGGATCAGAGTGACC 77
Db 82 CCACCAACCCCACTGTCTTACCAAGGCAAGAAAGCAATCCCGCGATCAGAGTGACC 141
Qy 78 GCCTTCTGATCAGAGGTGGAGGATCGTGAATGACGACCAAGTCTTTTACGCTGATGTGC 137
Db 142 GTCTCTTATCAAGGAGGAGCAGATGCTCAATGATGATCAGTCTTTTATGCTGATTT 201
Qy 138 AGGTGAAGATGGCTTGTATATAAACAATCGGAGAAACCTCATGCTCCCTGGGGGATCA 197
Db 202 ACATGAAGATGGCTTATAAACAATTTGGAGACAACTGTGATTTCTTCTGGAGGAGTGA 261
Qy 198 AGACCAATTCACCCCAAGCGCTGATGCTCTTCTGGTGGCTTGAGTCCACACAAGGC 257
Db 262 AGACCAATTAAGGCAATTTGGAAGATGTTGATCTCTGGAGGATCGATGCTCATCTACT 321
Qy 258 TGCAATGCTGTCTTGGGATGACACCGGCTGACGACTTCTGTCAGGGGACCAAGGCAG 317
Db 322 TCCAGATGCCATATAAGGGAATGACCAAGTAGATGACTTCTTCCAGGGACAAAGGGG 381
Qy 318 CGCTAGCAGAGGAACCAACATGATCTTGGACCACTCTTCCCGGACACGAGGTGAGCC 377
Db 382 CCTAGCAGTGGCACCAACATGATCATTTGACCATTTGCTGGCTGAGCTTCCAGCTCAG 441
Qy 378 TGCTGGGCGCTTACGAGCAGTGGCGGAGGCGGACAGCGGCGCTCTGTCGACTACT 437
Db 442 TGACTGAGGCTTATGAGAAATGGAGAGATGGGCTCATGGGAAGATTTGCTGTGACTATG 501
Qy 438 CCCTGCACGTGGACATCACCCGATGGCATGAGAGCATCAAGGAGGAGCTGGAGCCCTGG 497
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Db 502 ||||| CCCTGCAATGGAACATCACCCACTGGAATGACAGCGTCAAGCAGGAAGTGCAGAACTCA 561
QY 498 ||||| TCAAGAGAAAGGGTGTGAACCTCTCTCTGCTTCTATGGCATACAAGGACCGGTGCCAGT 557
Db 562 ||||| TCAAGGACAAAGGGTTAACTCTCTCTATGTTTATATGCTTATAGGATTTGTATCAG 621
QY 558 ||||| GCAGCGACAGCCAGATGTAAGAGATCTTACAGATCATCCGGGACCTGGGGCCCTTGGCCC 617
Db 622 ||||| TATCTAACACAGAGCTCTATGAGATCTTCACTGCTGGGAGAGCTGGGGGCCATTGCTC 681
QY 618 ||||| AGGTGCAAGTGAAGACGGGGACATCGTGGAGGAGGAGCAGAGCGGTTCCTGGAGTCG 677
Db 682 ||||| AAGTTCACTGCTGAGAAATGGGGATATCATGCCCCAGGAGCAAAACCCGCATGTGGAAATGG 741
QY 678 ||||| GCATCACTGGCCCCGAGGGCCACGTGCTCAGCCACACCCCGAGGAGGTGGAGCGG 737
Db 742 ||||| GGATACTGGCCCCAGAGGCCATGTAATGAGAGCGCCAGAGAGCTGGAAGCTGAGGCTG 801
QY 738 ||||| TGTAACGAGTGTACCATCGCCAGCAGGAACTGCCCGCTGTACGTCAACCAAGGTGA 797
Db 802 ||||| TGTTCGTGTCATCACCATTTGCCAGCCAAACCAATTTGCCCTCTCTACGTCAACAAAGTCA 861
QY 798 ||||| TGAGCAAGGGGGCGGCCGACGCCATCGCTCAGGCCAAGCCGAGGGGTGCTGTGTTTG 857
Db 862 ||||| TGAGCAAGAGTGCAGCTGACCTCATCTTCAAGCCAGGAAAGGAAATGTATGCTCTTTG 921
QY 858 ||||| GGAGGCCCATCACCGCCAGCTGGGACCGACGCTTCACTACTGAGCAAGCAACTGCGG 917
Db 922 ||||| GTGAGCCCATCACTGCCAGGCTTGGCATGATGAAACCCATTTATTTGGAGCAGAACTGGG 981
QY 918 ||||| CCAAGGCTGACGCTTCTGTCAATCACCTCACCTGTCACCCAGCAGCCACCAACCGGCGAGCC 977
Db 982 ||||| CCAAGGGGCTGCAATTTGTGACATCCCAACCCCTGAGCCCTGACCCCACTACTCCGGACT 1041
QY 978 ||||| ACCTACCTGCTGTGCTGCAGCGGGGACCTTCCAGGTGAAGGAGCGCCCACTGCACT 1037
Db 1042 ||||| ACATCAACTCTTGTGCTGGCCAGCGGGATCTGCACTATCTGGAGTGCCTCACTGCACT 1101
QY 1038 ||||| TCACCACTGCCAGAGGCTGTGGCAAGCAACTTGGCGCTGATCCCGAGGGCACCA 1097
Db 1102 ||||| TCAGCACTGCCAGAAAGCAATTTGGAAAGCAACTTTCAGCCATCTCTGAGGGCACCA 1161
QY 1098 ||||| ACGGCATTTGAGGAGCGCATGTGATGCTTGGGAGAAATGTGGCTCTTGGGAAGATGG 1157
Db 1162 ||||| ATGCTGTGGAGGAGCGCATGTCTCATCTTGGACAGGCTGTGGCCACAGGAAATGG 1221
QY 1158 ||||| ACGAGATGATGCTGTGCTGCGGTGACAGTACAAATGCTGCCAAATCTTCAATTTTACC 1217
Db 1222 ||||| ACGAAACCAAGTTGCTGTGCTGTGACAAAGCAAAACGCTGCCAAGATCTTCAACCTGTATC 1281
QY 1218 ||||| CAAGGAAGGGCGAGTGGCTGTGGGCTTCAAGCTGACCTGCTCATATGGAACCCCAAGG 1277
Db 1282 ||||| CCCGCAAGGGAAGAAATATCTGGGTTCTGACAGCGACCTCGTATCTGGGATCCAGATG 1341
QY 1278 ||||| CCACCAAGATCATCTCTGCCAAGACCACAATCTGAACTGGAGTACAAATCTTCGAGG 1337
Db 1342 ||||| CTGTGAGATCGTCTCTGCCAAGAACCAACAGTCTGGGCGAGTACAAATCTTTGAAG 1401
QY 1338 ||||| GATGTGAGTGCAGGGAGCGCTGCGGTGCTAATAGTCAAGGCGAGTGCAGCTGGAAG 1397
Db 1402 ||||| GGATGAGAGTGCAGGGGCTCTCTGTTGTGATCTGCCAGGGCGAAGATCATGCTGGAG 1461
QY 1398 ||||| ACGGAGAGATGTTTGTACCCCGGGGGCGGCTTCGTCCTTCGGAAGAAATTCGCCG 1457
Db 1462 ||||| ATGGCAACCTGCACTGACCGAGGGGCTGGCGCTTATACCTTGCAGCCGCTTCGCG 1521
QY 1458 ||||| ACTTTGTCTACAAGAGATCAAGCTCGCAACAGGCTGGCGGAGATCCAGCGTGTGCC 1517
Db 1522 ||||| ACTATGTCTACAAGCGCATTTAAGCAGCGGAGGAGATGGCAGACCTGCTGCCAA 1581
QY 1518 ||||| GTGGGCTGTATGACGGGCCGCTCCACGAGGTGATGCTGCTGCAACCGAGGAGTGGCG 1577

Db 1582 GGGGCATGTACGATGGGCGCTGTGTTTGACTGTACCAACCCCAAA---AGGTGGCACCC 1638
QY 1578 CTCCGGCCCGCGCTCTGCCCAGGCAAGATCTCCGTGCTCTGTGCGCAACTACATC 1637
Db 1639 CCGCAGGCTCTGCTCGGGGCTCTCCTACTCGGCGGAACCACTGTGAGGAATCTTCACTC 1698
QY 1638 AGTCGGGGTTCAGCCTATCTGGGTCTCAGGCTGATGA 1674
Db 1699 AGTCGGGATTTAGCTGTGAGGCAACCAAGTGGATGA 1735

RESULT 9

US-09-949-016-200
; Sequence 200, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 5047
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-200

Query Match 50.3%; Score 850.6; DB 4; Length 5047;
Best Local Similarity 70.0%; Pred. No. 2.4e-188;
Matches 1160; Conservative 0; Mismatches 494; Indels 3; Gaps 1;

QY 18 CCCCCAGGAGCAGGATGCTCTCCAGGGCGAAGAAAGCATCCCCCGGATCAGAGTGACC 77
Db 97 CCACCAACCCGCCACCATGTCTTACCAAGGCAAGAAAGCAATCCCGCGATCAGAGTGACC 156
QY 78 GCCTTCTGATCAGAGTGGAGGATCGTGAATGACCAAGTCTTTAGCTGATGTC 137
Db 157 GTCTCTTATCAAGGAGGAGGAGATCGTCAATGATGATCAGTCTTTATGCTGATTT 216
QY 138 ACGTGAAGATGGCTTTGATAAAACAAATCGGAGAAACCTCATCGTCCCTGGGGGATCA 197
Db 217 ACATGAAGATGGCTTAAATAAAACAAATTTGGAGACAATCTGATTTCTTGGAGGATGA 276
QY 198 AGACCAATTGACCGCCAGGCGCTGATGCTCTTCTGCTGGCTGTTGAGTCCACAAAGGC 257
Db 277 AGACCAATTGAAGCCAAATGGGAAGATGGTATCCCTGGAGGATCGATGTCCATCTCACT 336
QY 258 TGCAGATGCTGCTCTGGGCGATGACACCGCTGACCACTTCTGTCAAGGGCAACAGGCG 317
Db 337 TCAGATGCCATATAAGGGAATGACCACAGTAGTACTGCTTTCCAGGGCAACAGGCGG 396
QY 318 CGCTAGCAGGAGGAACCAACATGATCTTGGACCAACCTCTTCCCGGACACCGGGTGTGAGCC 377
Db 397 CCTTAGCAGGTGGCACCAACCATGATCATTTGACCAATGTGGTCTGAGCTGAGTCCAGCC 456
QY 378 TGTGCGGCGCTACGAGAGAGTGGCGGAGCGGCGGACGCGCGGCTGTCTGCACTACT 437
Db 457 TGACTGAGGCTATGAGAAATGAGAGAGTGGGCTGATGGGAAGAGTTGCTGTGACTATG 516
QY 438 CCTGCACTGTGACATCACCGATGCTGAGAGATCAAGGAGGAGCTGGAGCCCTGG 497
Db 517 CCTGATGTGGACATCACCCACTGGAATGACAGCGTCAAGCAGGAGTGCAGAACCTCA 576
QY 498 TCAAGGAAGAGGTGTGAACTCTCTCTGCTTTTCATGGCATACAAGGACCGGTGCCAGT 557

Db 577 TCAAGGACAAAGGGTTAACTCTTATGTTTATATGGCTTATAAGGATTTGTATCAAG 636
Qy 558 GCAGCAGCAGCAGATGTACAGATCTTACAGATCATCCGGGACCTGGGGGCCCTTGGCCC 617
Db 637 TATCTAACACAGAGCTCTATGAGATCTTACCTGCTGGGAGAGCTGGGGGCCCTTGTCTC 696
Qy 618 AGGTGACCGCTGAGAACGGGGACATCGTGGAGGAGGACAGAGCGGTTGCTGGAGCTCG 677
Db 697 AAGTTTATGCTGAGATGGGGATATCATTTGCCAGGAGCAAAACCCGCATGTTTGGAAATGG 756
Qy 678 GCATCACTGGCCCCGAGGGCCAGCTGCTCAGCCACCCCGAGGAGGTGGAGGCTTGAGCGG 737
Db 757 GGATACTGGCCAGAGGCCATGTACTGAGCAGGCCAGAGAGCTGGAGCTGAGGCTG 816
Qy 738 TGTACCGAGCTGTCACTATCGCAAGCAGGCAAACTGCCCGCTGTACGTCAACCAAGGTGA 797
Db 817 TGTTCGGTGCATCAGCATTTGCCAGCAAAACCAATTGGCCCTCTCTACGTCACAAAAGGTCA 876
Qy 798 TGAGCAAGGGGGCGGCGGAGCCATCGCTCAGGCCAAGCGCAGAGGGGTGGTCTGTTTG 857
Db 877 TGAGCAAGAGTGCAGCTGACCTCATCTCAAGCCAGGAAAAAGGAAATGTTAGTCTTTG 936
Qy 858 GGAGGCCCATCACCGCAGCTGGGCACCGACGGTTTCACTACTGGAGCAAGAACTGGG 917
Db 937 GTGAGCCCATCACTGCAGGCTCGGATAGTAGTGAACCCATTTATTTGAGCAAGAACTGGG 996
Qy 918 CCAAGGCTGAGCTTGTGTCATCATCCCGCTGTCAACCCAGACCCCAACCGGAGACC 977
Db 997 CCAAGGCGGTGCTTTTGTGACATCCCAACCCCGTGGCCCTGACCCAACTACTCCGGACT 1056
Qy 978 ACCTGACCTGCTGCTGCTCCAGGGGGACCTTCAGGTGACAGCAGGCGCCACTGCACCT 1037
Db 1057 ACATCAACTCTTGTGCTGGCAGCGGGGATCTGCAGCTATCTGGGAGTGCCCACTGCACCT 1116
Qy 1038 TCACCACTGCCAGAGAGGCTGTGGGCAAGGACAACTTTCCGCTGTATCCCGGAGGCAACA 1097
Db 1117 TCAGCACTGCCAGAAAGCAATTTGGGAGGACAACTTCACAGCCATTCCTGAGGCAACA 1176
Qy 1098 ACGGCATTGAGGAGCGGATGTGATGGTCTGGGAGAAATGTGGCTCTTGGGAAAGTGG 1157
Db 1177 ATGGTGTGGAGAGCGGATGTCTGTCTATCTGGGACAAAGCTGTGGCCACAGGGAAAAATGG 1236
Qy 1158 ACGAGATGAGTTGCTGCGGGTACAGATACAAATGCTGCGCAAAATCTTCAATTTTACC 1217
Db 1237 ACGAAACCAAGTTGCTGGTGTGACAAAGCAAAACGCTGCAAGATCTTCAACCTGTATC 1296
Qy 1218 CAAGGAAGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGTGTCATATGGAACCCCAAGG 1277
Db 1297 CCGCAGAGGAGAGAAATATCTGTGGGTTCTGACAGCAACCTGCTCATCTGGGATCCAGATG 1356
Qy 1278 CCAACAGATCATCTCTGCCAAGACCCACAACTCTGAACTGGAGTACAACATCTTCGAGG 1337
Db 1357 CTGTGAAGATCGTCTCTGCCAAGAACCAACAGCTGCGGACAGATGACAACTCTTTGAAG 1416
Qy 1338 GAGTGAAGTCCGGGAGCGCTGCGGTGTGATTAAGTCHAGGCGCGAGTGCGCGCTGGAGG 1397
Db 1417 GGATGAGCTGCGCGGGCTCTCTGTTGTGTCATCTGCCAGGGAAGATCATGCTGGAAG 1476
Qy 1398 ACGGGAAGATGTTTGTACCCCGGGGGCGGGCGCTTCTGCTCCGGAAGAAACATTCGCCG 1457
Db 1477 ATGGCAACTGTCAGCTGAACCGAGGGCTGGCGCTTTCATACCTGACGCCGCTTCTCGG 1536
Qy 1458 ACTTTGTCTACAAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGCTGTGCCCC 1517
Db 1537 ACTATGCTACAAAGCGCATTAAGCAACGAGGAAGATGGCAGACCTGCGATGCCGTCCCAA 1596
Qy 1518 GTGGGCTGTATGACGGGCCCGTCCACGAGTGTGTGCTGCTGCAAGCCAGGAGTGCGG 1577
Db 1597 GGGGCGATGTACGATGGGCTGTGTTGACCTGTGACCCACCCCAAC---AGTGGGCAACCC 1653
Qy 1578 CTCGGGCCCGCGCTCTCTGCCAGGCAAGATCTCCGTGCTCTCTGTGCGCAACCTACATC 1637

Db 1654 CCGCAGGCTCTGCTCGGGGCTCTCTACTCTCGGCCGAACCCACTGTGAGGAATCTTTCATC 1713
Qy 1638 AGTCGGGTTTACGCTATCTGGGTCTCAGGCTGATGA 1674
Db 1714 AGTCGGGATTTAGCCTGTCCAGGCACCCCAAGTGGATGA 1750
RESULT 10
US-09-976-594-131
; Sequence 131, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 131
; LENGTH: 3331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 408751.3
US-09-976-594-131

Query Match 30.9%; Score 521.8; DB 4; Length 3331;
Best Local Similarity 59.0%; Pred. No. 8.1e-112;
Matches 951; Conservative 0; Mismatches 657; Indels 5; Gaps 3;
Qy 69 CGAGTGACCGCTCTTGATCAGAGGTGGGAGGATCGTGAATGACGACCAAGTCTCTTTTACG 128
Db 66 CCAGCGTGAGGATCTCATCAAGGGAGGCAAGTGTGAAACGATGACTGCACCCACGAGG 125
Qy 129 CTGATGTGCACTGGGAAGATGCTTGATATAAAACAAATCGGAGAAACCTCATGTCCTCTG 188
Db 126 CTGACGCTTACATCGAAGATGGCATCATCCAGAGGTGGCGCGGAGCTCATGATCCCTG 185
Qy 189 GGGGCATCAAGACCATTTGACGCCACCGCTGATGGTCTCTCTGGTGGGTTGAGCTCC 248
Db 186 GCGGGGCCAAGGTGATTGATGCCACAGGAAACTTGTGATCCTCTGGTGGATCGACACCA 245
Qy 249 ACACAGGCTGCAGATGCTCTCTGGGATGACACCGGCTGACGACTTCTGTACGGGCA 308
Db 246 GCACCCACTTCCACAGACTTTCATGAATGCCACGTCGTGGACGACTTCTACCATGGGA 305
Qy 309 CCAAGCAGCGCTAGCAGGAGGAACCAACATGATCTTGGACCAACGCTTCTCCCGCACCGG 368
Db 306 CCAAGCAGCACTCTGTCGGAGGACCAACCATGATCATCGGCCACGCTCTGCCGCAAGG 365
Qy 369 GTGTGAGCTCTGTCGGCGCTTACGAGCAGTGGGGAGGCGGGCGGAGCAGCGGCGCTGCT 428
Db 366 AGACCTCCCTTGTGGACGCTTATGAGAACTGCGGAGTCTGCGCGACCCCAAGGTCTGCT 425
Qy 429 GCGACTACTCTGACGCTGGACATCACCCGATGGCATGAGAGCATCAAGGAGGAGCTGG 488
Db 426 GTGATTACGCCCTTCCACGTGGGATCACCTGTGGGACCCCAAGGTGAAGCAAGTGG 485
Qy 489 AGGCCCTGTCAAGGAGAAAGGTGTGAATCTCTCTCTGTTCTTTCATGGCATCAAGGACC 548
Db 486 AGACACTGGTGGAGGAGAGGGTGTCAACTCTGTTCCAGATGTTTCATGACCTACAGGACC 545
Qy 549 GGTGCCAGTGCAGCAGCCAGATGTACAGATCTTTCAGCATCATCCGAGACCTGGGG 608
Db 546 TGTATCATGTTCTGAGACAGTGAGCTGTACCAAGTGTTCACGCTTGCAGGACATTGGGG 605
Qy 609 CTTTGGCCCGGCTGACGCTGAGAACCGGAGCATCGTGGAGGAGGAGCAGAGCGGTTGC 668

Db 606 CAATCGCCCGCTCCATGCTGTAATAATGGGGAGCTTGTGGCGGAGGGTGCTTAAGAGGCAC 665
Qy TGGAGCTCGGCATCACTGGGCCCGGAGGGCCACGCTGCTCAGCCACCCCGAGGAGGTGAGG 728
Db TGGATTTGGGGATCACAGGCCAGAGGATCGAGATCAGCCGTCCAGAGGAGCTGGAAG 725
Qy CTGAGGGCGGTATCCGAGCTGTCTCAATCGCCAAAGCAGGAACTGCGCCGCTGTACGTCA 788
Db CTGAAGCCACTCATCTGCTGTATCAACCATGCAACAGGACTCACTGTCTCAATCTACCTGG 785
Qy CCAAGGTGATGAGCAAGGGGCGCCGACGCCATCGCTCAGGCCCAAGCGCAGAGGGGTGG 848
Db TCAAGCTGTCAAGTATCTGGCTGGTCAAGCTTATCGAGCTGTCAAGTCAAGGGGAGG 845
Qy TCGTGTGTGGGAGCCCATCAACGCCAGCCCTGGGCAACCGGTTTCACTACTCTGAGCA 908
Db TTGTGCTGGCGGAGACCACTGACATGCCATGCCCTGACAGGCTTACACTACTACCAAC 905
Qy AGAATGGGCCAAGGCTGAGCCTTCTGTAC - ATCACCCTCTGTCAACCCAGAGCCCAAC 967
Db AGGACTGGTCCACGCGGCTGCTTATGTCAAGGTGCTTCCGCTGAGACTGGACACCAAC 965
Qy ACGCAGACCACTCACTGCTGCTGTCTGCTCAGCGGGGACCTCCAGGTGACAGGCGAGGCC 1027
Db ACTCAACCTCACTATGAGCTGCTGTGCTCAATGACACTCTGAACATCTGTGGCATCAGAT 1025
Qy CACTGCACTTTCACCACTGCCAGAGGCTGTGGGCAAGGACAACTTTCGGGCTGATCCCC 1087
Db CACGGCCTTTCACCACAATCAGAAAGCTATGGGCAAGGAGACTTTCACCAAGATCCCA 1085
Qy GAGGCAACCAAGGCTATGAGGAGCGCATGTGATGCTGTGGAGAAATGTGTGGCCTCT 1147
Db CATGGAGTGTGCTGCTGAGGACCGCATGAGGCTCATCTGGGAGAGAGGAGTGTGGGA 1145
Qy GGGAAGTGAACGAGATGATGTGCTGCGGTGACAGTACAAATGTGTCAAATCTTC 1207
Db GGAAGATGATGAGAAACCGTTTGTGGCCGTACCAAGTTCCCAACGAGCTTAAGCTTCTG 1205
Qy AATTTTTCACCAAGAGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGTGCTCATATGG 1267
Db AACCTGTATCCCGCAGGGCCGATTAATTCGGGAGCGGATGCTGATGTGTGGTGG 1265
Qy AACCCAAAGGCAACCAAGATCATCTGTGCCAAGACCCACAAATCTGAAGTGTGGAGTCAAC 1327
Db GACCCAGAGGCCAACAAAGACCATCTCAGCCAGCAGCAGGCTCAGGGAGGAGACTTCAAC 1325
Qy ATCTTCAGGAGGTGGAGTGGCGGAGCGCTGCTGCTGATGATGATGATGATGATGATGATG 1387
Db CTGTATGAGAAACATGCGCTGCCACGCGGTGCCACTGTGCTCAACCATCAGCCGCGGCGCTC 1385
Qy GCGCTGAGGACCGGAAAGATGTTGTCAACCCGGGGGCGGCGCTTCTGCTCCCTCGGAA 1447
Db GTGAT - GAGAAAGCGGCTTTCATGTGCGCGGAGGGGACCGGCAAGTCTGTCTCCCTGAGG 1444
Qy ACATTCGGAATTTGTCTAAGAGGATCAAGAGCTCGCAACAGGCTGCGGAGATCCAC 1507
Db TCCTTCCAGACACTGTCTACAAAGAGCTGTGTCAGAGAGAGAACTTTAAAGGTAGA 1504
Qy GTGTGCCCCGTGGCTGTATGAGCGGCGCTGCTCAAGAGTGTGTCCTGCGCTGCAAGCCA 1567
Db GGAGTGGACCGCACTCCCTACCTGCGGGGATGTGCTGTTGTGCTGCAACCTTGGGAAAAA 1564
Qy GCGAGTGGCGCTCGCGGCGCTGCTGCGGCAAGGATCTCGGCTGCTGCTGCTGCTGCTGCTG 1624
Db GAGTGGGAACCCCACTGCGAGACATCTCAACCGGCGGCTCAACCGGCAATGGGGCATG 1624
Qy CGCAACTCATCAGTGGGGTTGAGCCTTATCTGGGTCTCAGGCTGATGACCA 1677
Db ACGGACCTTCACGAATCCAGCTTCAGGCTCTCTGCTGCTCTCAGATCGATGACCA 1677

RESULT 11

US-09-252-991A-6970

; Sequence 6970, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; LENGTH: 1524

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-6970

Query Match 23.0%; Score 389.2; DB 4; Length 1524;

Best Local Similarity 56.2%; Pred. No. 4.8e-81;

Matches 774; Conservative 0; Mismatches 598; Indels 6; Gaps 2;

Qy 79 CCTTCTGATCAGAGGTGGGAGGATCGTAATGACGACCACTCTTTTACGCTGATGCA 138
Db 90 CTTGTGATCCGTGGGCGCACCGCTGTTACTTCAAGAGAGATTATCGAGCCGACGTCT 149
Qy 139 CGTGGAGATGCTTCAATAAACAATCGGAGAAACCTCATCGTCCCTGGGGGCATCAA 198
Db 150 CTGTGCCAACGGCTTATCCAGGCCATCGCGGAGAACTTCGAAACCCCTTCCGGCTGCGA 209
Qy 199 GACCATTTGACGCCACGCGCTGATGCTTCTTCTGCTGGGCTTGAAGTCCACCAAGGCT 258
Db 210 CGTCTCTGACGGGGTGGCCAGTACCTGATCGCGGGCGGATCGACCCCATATCCACAT 269
Qy 259 GCAGATGCTGTCTGGGATGACACCGGCTGACGACTTCTGTCAAGGCAACCAAGGAGC 318
Db 270 GCAGTTGCTTCTCATGGCAGCGTGGCCAGCGAGGACTTCTTCAGGGGCAACCGGCGCG 329
Qy 319 GCTAGCAGAGGAGAACCAACCATGATCTTGGACCACTTTCCTCCCGCACACGGGTGAGCCT 378
Db 330 GCTGGCGGAGGAGCAACCTCGATCATCGATTCCTGCTCATCCCCCAACCCGCGACGCTCGCT 389
Qy 379 GCTGGCGGCTTACGACGAGTGGCGGAGCGGCGGACAGCGCGCTGCTGCGACTACTC 438
Db 390 GCTGGAGGCTTTCACACCTTGGCGCGCTGGGCGGAGAAATCCGCTGCG ---GACTACGG 446
Qy 439 CTTGCACTGGAATCACCCGATGGCATGAGAGCATCAAGGAGGAGCTGGAGGCGCTTGT 498
Db 447 CTTCCACGTCGCCATCACCTGTTGGAGCGACGAGGTGCGCCGGGAAATGGGCGAGCTGGT 506
Qy 499 CAAGGAGAGGGTGTGAATCTTCTTCTGCTTTCATGGCATACAAGGACCGGTGCCAGTG 558
Db 507 GGCACAGCAGGGGTGAAACAGCTTCAAGCACTTCATGGGCTTACAGAACGCCCATCATGGC 566
Qy 559 CAGCGACAGCCAGATGTAGAGATCTTACGATCATCTCGGAGCTTGGGGCTTGGGCCA 618
Db 567 GCGCGAGATACCTGCTGGTGGCCAGCTTTCAGCGCTGCTGGAGCTGGGCGGCTGCCGAC 626
Qy 619 GGTGCACTGAGAACCGGGGACATCGTGGAGGAGGAGAGGAGCGGTGTCTGGAGCTCGG 678
Db 627 GGTGCACTGAGAACCGGGGACATCGTGGTCTTCCACCTTCCAGGAGGAGAACTCTCGCC 686
Qy 679 CATCACTGGGCGGAGGCGCATGCTGCTCAGCCACCCCGAGGAGGTGGAGGCTGAGCGGT 738
Db 687 CTTACCGGCGGAGGCGCATCTCTGCTGCGCTCCGCGCAAGTCCAGGCGGAGGCGCGC 746
Qy 739 GTACCGAGCTGTCAACCATCGCAAGCAGGCAAACTGCTGCTGCTGCTGCTGCTGCTGCT 798
Db 747 CAGCCGCGCATCCGCATCGCCGAGAGCTGGGGTACGCCCTGTACTCTGCTGCTATTTTC 806
Qy 799 GAGCAAGGGGCGGCGCGGACGCCATCGCTCAGGCCAAGCGCAGAGGGGTGCTGCTGTTGG 858

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Db 807 CAGCCGCGAGGCGCTGGAAGATCGCTATGCCCCGCGCAAGGCGCCAGCGGCTCTACGG 866
Qy 859 GGAGCCCATCAGCCGAGCTGTGGCAACGACGGTTCACTACTGAGGCAAGAACTGGGC 918
Db 867 CGAGTGTCTGGCGGGGACCTTGCTGCTCGACGACAGCGTCTACCGCGCACCCGAGCTGGGC 926
Qy 919 CAAGGCTGAGCCCTTGGTCATACCCCTGTCAACCCAGACCCCAACACGCGACACCA 978
Db 927 CACCGGGCGGATACGTATGAGCCCGCGTTCCGTCCGTCGAACACAGGAAGCGCT 986
Qy 979 CTTCACTGTCTGCTTCAGCGGGGACCTTCAGAGTGACAGGCGAGCGGCCCACTGCACCTT 1038
Db 987 GTGGCGGGCTCGAGTCCGGCA--ACCTGCATACACCGCACCGCACTGCTGCTT 1043
Qy 1039 CACCACTGCCAGAGGCTGTGGGCAAGACAACTTCGGCGCTGATCCCGAGGGGCAACCA 1098
Db 1044 CTGGCGCGAGCAGAGGCCATGGGCGCGACGACTTCAGCAAGATTTCCCAATGGCACGGC 1103
Qy 1099 CGGCATTGAGGAGCGCATGTGATGTCTGGGAGAAATGTGTGGCTCTGGGAGATGGA 1158
Db 1104 CGGCATCGAGGACCGCATGGCTGTCTGTGGGACCGCGGGTCAACAGCGGGCGCTGTG 1163
Qy 1159 CGAAGATGAGTTGCTCGCGGTGACCAAGTACAAATGCTGCCAAATCTTCAATTTTACCC 1218
Db 1164 GATGCACGAGTTGCTCGCGTGACTCCACCAACACCGGAAGATCTTCACTGTTCCT 1223
Qy 1219 AAGGAAGGGCGAGTGGCTGTGGCTGTGACGTGACCTGTGATATGAAACCCCAAGGC 1278
Db 1224 GCGCAAGGGCGGATCGCGCTCGCGCGGATGCGGACCGACTGTGCTCTGGGACCGGAGG 1283
Qy 1279 CACCAAGATCATCTCTGCCAAGACCCACCAATCTGAAGCTGAGTACAAATCTTCGAGGG 1338
Db 1284 CAGCCGACCTCTCGCGCGCCACCCATACAGCGGGTGCATTTCAACATCTTCGAAGG 1343
Qy 1339 AGTGAAGTGC CGGGGAGCGCTCGCGTGTGTCATAAGTCAAGGCGCGAGTGGCGCTGGAGGA 1398
Db 1344 TCGCACCGTGGCGGATNTCCAGCACACCACTCAGCCAGGGAAGCTGCTCTGGGCGC 1403
Qy 1399 CGGGAAGATGTTTGTACCCCGGGGGCGCGCTTGTCTCCCTCGGAAACATTTCCG 1456
Db 1404 AGCGACCTGGCGCGCAACCGCGCGGACGCTAGTGGAGCGCGCGCTTACCGC 1461
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RESULT 12

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US-09-252-991A-6924
; Sequence 6924, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6924
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6924
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Query Match 23.0%; Score 389.2; DB 4; Length 1611;
Best Local Similarity 56.2%; Pred. No. 4.9e-81;
Matches 774; Conservative 0; Mismatches 598; Indels 6; Gaps 2;

Qy 79 CTTCTGATCAGAGTGGGAGGATCGTGAATGACGACCACTCTCTTTTACCTGATGCA 138
Db 79 CTTGTTGATCCGTGGGCGCACCGTGGTGTACTACGAAGAGATTTATCGAGCCGACGTGCT 138
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Qy 139 CGTGAAGATGCTTGTATAAACAATCGGAGAAACCTCATCGTCCCTGGGGGCATCAA 198
Db 139 CTGTGCAACGCGCTCATCCAGGCCATCGCGAGAACCTCGAAACCCCTCCGCGTCCGA 198
Qy 199 GACCAATTGACGCCACGCGCTCATGCTCTTCTGTGTGGCGTTGACGTCCACACAAAGGCT 258
Db 199 CTTCTCGACGGGGTGGCCAGTACTGTATGCGGGGGCATCGACCCCCATACCCACAT 258
Qy 259 GCAGATGCTGTCTGGGGATGACACCGGCTGACGACTTCTGTCTAGGGGACACGAGGCGC 318
Db 259 GCAGTGTGCTTCTAGGGGACGCTGGCCAGCGAGGACTTCTTTCAGCGGCAACCGCGCGG 318
Qy 319 GCTAGCAGAGGAAACCACTATGATCTTGACCAACGCTTCTCCCGACACAGGCTGTGAGCT 378
Db 319 GCTGGCGGAGGAGCACCTCGATCATGACTTCTGTCATCCCCAACCCCGGACAGTCGCT 378
Qy 379 GCTGGCGGCTACGAGCAGTGGCGGAGCGGCGGACAGCGGGCGCTGTGCGACTACTC 438
Db 379 GCTGGAGGCTTCCACACCTGGCGGCTGGGGCGAGAAATCCGCTGCG--GACTACGG 435
Qy 439 CTTGCACTGTGGAATCACCCTGATGGAATGAGAGCATCAAGAGAGAGCTGAGGCTCTGCT 498
Db 436 CTTTCACTGCTGCGCATCACCTGCTGAGCGACGAGGTGCGCCGCGAAATGGCGAGCTGT 495
Qy 499 CAAGGAGAGGCTGTGAATCTCTTCTGTCTTCTGTCATGGCATACAGGACCGGTGCCAGTG 558
Db 496 GGCACAGCAGCGGGGTGAACAGCTTCAAGCACATTCATGGCTTCAAGAAACGCGCATATGGC 555
Qy 559 CAGCGACAGCCAGATGTACGAGATCTTCAGCATCATCCGGGACCTGGGGGCGCTTGGCCCA 618
Db 556 CGCGGACGATACCTTGGTGGCCAGCTTTCAGCGCTGCTGAGAGCTGGGCGCGGTGCCGAC 615
Qy 619 GGTGCACTGTGAGAACGGGGAATCTGTGAGAGGAGAGAGAGCGGTTCTGTGAGTCTGG 678
Db 616 GGTGCACTGAGAGAACGGGGAATCTGTCTTTCACCTGACGAGAGAACTCTCTGCCAGGG 675
Qy 679 CATCACTGCGCGCGGAGGCGCACGTGCTCAGCCACACCCCGAGGAGGTGAGGCTGAGCGGT 738
Db 676 CTTTACCGCGCGCGAGGCGCATCTCTGTGCGCTGCGCGCAAGTGAAGGCGAGGCGCGC 735
Qy 739 GTACCGAGCTGTCAACCATCGCCAAAGCAGGCAAACTGCGCGCTGTACGTCAACAAAGTGTAT 798
Db 736 CAGCGCGCATTCGCGATCGCGGAGCTGGGTAGCGCGCTGTACTGTGTGATATTTC 795
Qy 799 GAGCAAGGGGGGCGCGACCGCATCTGAGGCAAGCGCAGAGGCGGTGCTGTGTTGG 858
Db 796 CAGCGCGAGGCGCTGGACGAGATCGCTTATGCGCGCGCAAGGGCGAGCGGCTCTACGG 855
Qy 859 GGAGCCCATCAGCGCGAGCTGGGCACCGAGGTTCACTACTGAGCAAGAACTGGGC 918
Db 856 CGAGTGTCTGGCGCGGCACTTGTGTCGACGACAGCGTCTACCGGCAACCGGAGCTGGGC 915
Qy 919 CAAGGCTGAGAGCTTCTGTCACTACACCCCTGTCAACCCAGACAGCCCAACGCGCAGACCA 978
Db 916 CACCGCGCGGATAGTGTATGAGCCCGCGCTTCCGTCCGTCGAACACAGGAAGCGCT 975
Qy 979 CTTCACTGTCTGTCTCAGCGGGGACCTTCAGAGTGACAGGCGAGCGCCCACTGTGACCTT 1038
Db 976 GTGGCGCGGCTGCACTCGCGCA--ACCTGATACACCGCGCACGACCACTGTGCTT 1032
Qy 1039 CACCACTGCGCAGAGGCTGTGGGCAAGGACGACACTTTCGCGCTGATCCCGGAGGCGACCA 1098
Db 1033 CTGGCGCGGAGCAGAGGCCATGGGCGCGACGACTTTCAGCAAGATTTCCCAATGGCAGGC 1092
Qy 1099 CGGCATTGAGGAGCGCATGTGATGCTGTGGGAGAAATGTGTGGCTCTCTGGGAAGATGGA 1158
Db 1093 CGGCATCGAGGACCGATGCGCTGTGTGGGACCGCGGGGTCAACAGCGGGCGCTGTC 1152
Qy 1159 CGAAGATGTTGCTGTGCGGCTGACGATGATCAAAATGTGCGCAAAATCTTCAATTTTACCC 1218
Db 1153 GATGCAAGATGCTGCTGCGCTGACCTCCACCAACACCGCGAAGATCTTCAACCTGTTC 1212
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QY 1219 AAGGAAGGCGAGTGGCTGTGGGCTGTGACGCTGACCTGTGTATATGGAACCCCAAGGC 1278
Db |||||
QY 1213 GCGCAAGGCGCGATTCGCGCTGCGCGGATGCGGATGCGGATGCTGTGCTGTGGACCGCAGGG 1272
Db |||||
QY 1279 CACCAAGATCATCTCTGCAAGACCCACAACTCTGAACTGTGAGTACAACTCTTCGAGGG 1338
Db |||||
QY 1273 CAGCGCACCTCTCTGCGCGCCACCATCATCAGCGGGTGTATTTCAACATCTTCGAAGG 1332
Db |||||
QY 1339 AGTGAAGTGGCGGAGAGCGCTGCGTGTGTATAGTCAAGGCGCGAGTGGCGCTGAGGA 1398
Db |||||
QY 1333 TCGCACCTGTGCGCGCATTCACAGCCACCATCAGCCAGGCAAGTGTCTCTGGGCGC 1392
Db |||||
QY 1399 CGGGAAGATGTTGTACCCCGGGGGCGCGCTTGTCTCCCTCGGAAACATTCGCG 1456
Db |||||
QY 1393 AGGCGACTGTGGCGCGAACC CGCGCGCGAGCTAGCTGAGAGCGCGGCTACCG 1450
Db |||||

RESULT 13

US-09-252-991A-6769/c
; Sequence 6769, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6769
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6769

Query Match 23.0%; Score 389.2; DB 4; Length 1782;
Best Local Similarity 56.2%; Pred. No. 5.1e-81;
Matches 774; Conservative 0; Mismatches 598; Indels 6; Gaps 2;

QY 79 CTTCTGATCAGAGTGGGAGGATCGTAATGACGACAGTCTCTTTAAGCTGATGCA 138
Db CTTGTTGATCGGTGGCGCCACCGTGTACTCAGAGAGAGATTATCGAGCCGAGTGTCT 1601
QY 139 CGTGAAGATGGCTTGTATATAAACAATCGAGAAACCTCATGCTCCCTGGGGGATCAA 198
Db CTGTGCCAACGGCTCTATCCAGGCCATCGCGGAGAACCTCGAAACCCCTCCGCTGCGA 1541
QY 199 GACCATGAGCCGACCGCTGATGCTCTTCTGTGGGGTGTGAGCTGCCACCAAGGCT 258
Db CGTCTCGACGGGTGGCGAGTACCTGATGTCGCGGCGGATGACCCCATCCACAT 1481
QY 259 GCAGATGCTGTCTGCGGATGACACCGGTGACGACTTCTGTGAGGCAACCAAGGCG 318
Db GCAGTTGCCCTTCATGGGACGGTGGCGGACGAGGACTTCTCAGCGGCAACCGGCGG 1421
QY 319 GCTAGCAGGAGAACCAACATGATCTTGGACAGCTTCTCCCGACACGCGGTGTGAGCT 378
Db GCTGGCGGAGGAGAACCACTCTGATCATCTGCTATCTCCCAACCCCGGACAGTGTCT 1361
QY 379 GCTGGCGGCTTACGAGCAGTGGCGGAGCGCGGAGCGCGCTGCTGCGACTACTC 438
Db GCTGGAGGCTTCCACACCTGGCGGCTGCGGCGAGAAATCGCTGCG---GACTACGG 1304
QY 439 CTTGACGTGGATCATCCCGATGGATGAGAGCATCAAGGAGGAGCTGAGGCGCTGTGT 498
Db CTTCCAGCTGCCATCACCCTGTGGAGCAGAGGTGCGCGGGAATGGCGAGTGTGT 1244
QY 499 CAAGGAGAGGGTGTGACTCTCTTCTGCTTCTCATGGCATAAAGGACCGGTGCCAGTG 558
Db |||||

RESULT 14

US-09-949-016-5326
; Sequence 5326, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

Db 1243 GGCAACAGACGGGGTGAACAGCTTTCAAGCACTTCATGGCCTTCAAGAACGCCATCATGGC 1184
QY 559 CAGCGACAGCAGCATGATGACGAGATCTTTCAGCATCATCCGGGACCTGGGGGCTTTGGCCCA 618
Db |||||
QY 1183 CCGCGACGATACCTTGTGTGCGGAGCTTTCGAGCGCTGCTGAGAGTGGGCGGCTGCGAC 1124
Db |||||
QY 619 GTGTCAGCTGTAGAAACGGGACATCTGTGAGAGGAGAGCAGAACGGTGTGTGAGCTCGG 678
Db |||||
QY 1123 GTGTGACGCGGAGAAACGGGAACTGTGTCTTCCACTGACAGCAGAAACTCTCTCGCCAGGG 1064
QY 679 CATCACTGGGCGCGGAGGCGACGCTGTGACGACCCCGAGGAGGTGAGGCTGAGGCGGT 738
Db |||||
QY 1063 CTTACCGGCGCGGAGGCGCATCTCTGTGCTGCGCTCCCGCAGGTTCGAGGCGGCGCGC 1004
QY 739 GTACCGAGCTGTCAACATCGCCCAAGCAGGCAAACTGCGCGCTGTACGCTCAACAAAGTGTAT 798
Db |||||
QY 1003 CAGCGCGGCGCATCGCATCGCGAGAGCTGGGTACGCGCTGTACTGTGTGCAATTTTC 944
QY 799 GAGCAAGGGCGCGCGACGCCATCGCTCAGGCCAAGCGAGAGGGGTGTGTGTGTTGG 858
Db |||||
QY 943 CAGCGCGAGGCGCTGTGACGAGATGCGCTATGCGCGCAAGGGCGCAGCGGTCTACGG 884
QY 859 GGAGCCCATCAGCGCGAGCTTGGCAGCGGCTTCACTACTGAGGAGCAAGACTGGGC 918
Db |||||
QY 883 CGAGGTGTGCGCGGCGCACCTGTGTGACGACAGCGTCTACGCGCACCGGACTGGGC 824
QY 919 CAAGGCTGACGCTTGTGTACATCACCCCTGTCAACCCAGAGCCACACCGGCGAGACCA 978
Db |||||
QY 823 CACGCGCGCGGATACGTGATGAGCCCGCGCTTCCGTCCTGACACACAGGAGCGCT 764
QY 979 CTTCACTGTCTGTGTTCAGCGGGGACCTTCCAGGTGACAGGCGCGCCCACTGTGACCTT 1038
Db |||||
QY 763 GTGCGCGGCTGTGCTGCTCGGCA--ACCTGCATACCAACCGCCACCGGACTGCTGCTT 707
QY 1039 CACCACTGCCAGAGGCTGTGGGCAAGGACAATCTTCCGCTGTATTCGCGGAGGCGACCAA 1098
Db |||||
QY 706 CTGCGCGGAGCAGAGGCGCATGGGCGCGGACGACTTTCAGCAAGATTCCCAATGCGACGGC 647
QY 1099 CGGCAATTGAGGCGGATGCTGATGCTGCGGAGAAATGTGCGCTCTGCGAAGATGGA 1158
Db |||||
QY 646 CGGCACTGAGGACCGATGCGCTGTGTGGAGCGCGGGGTCAACAGCGGCGGCTGTGTC 587
QY 1159 CGAAGATGATGCTGCTGCGGTGACCAAGTACAAATGTGCGCAAAATCTTCAATTTTACCC 1218
Db |||||
QY 586 GATGACGAGTTCGTGCGCTGACCTCCACCAACACCGCGAAGATCTTCAACCTGTTCCC 527
QY 1219 AAGGAAGGCGAGTGGCTGTGGGCTGTGAGCTGACCTGTGTATATGAAACCCCAAGGC 1278
Db |||||
QY 526 GCGCAAGGCGGATCGCGTCCGCGGATGCGGACCTGCTGTGGGACCGCGCAGGG 467
QY 1279 CACCAAGATCATCTTGCACAGACCCACCAATCTGAAAGCTGAGTACAACTTTCGAGGG 1338
Db |||||
QY 466 CAGCGGACCTCTCGCGCGGCGGATCCCATCACCAGCGGTGATTTCAACTTTCGAAGG 407
QY 1339 AGTGAAGTGGCGGAGCGGCTGCGCTGTGCTATAAGTCAGGCGCGGCTGCGAGGA 1398
Db |||||
QY 406 TCGCACCGTGGCGGATTTCCAGCCACACCATCAGCCAGGCAAGCTGTCTCTGGGCGC 347
QY 1399 CGGGAAGATGTTGTACCCCGGGGGCGGCGCTGCTGCTCCCTCGGAAACATTTCCCG 1456
Db |||||
QY 346 AGGCGACCTGCGCGCGGAAACCGCGCGGACGCTAGCTGAGGCGCGCGCTACCGC 289
Db |||||

		CURRENT FILING DATE: 2000-04-14			
		PRIOR APPLICATION NUMBER: 60/241,755			
		PRIOR FILING DATE: 2000-10-20			
		PRIOR APPLICATION NUMBER: 60/237,768			
		PRIOR FILING DATE: 2000-10-03			
		PRIOR APPLICATION NUMBER: 60/231,498			
		PRIOR FILING DATE: 2000-09-08			
		NUMBER OF SEQ ID NOS: 207012			
		SOFTWARE: FastSeq for Windows Version 4.0			
		SEQ ID NO 5326			
		LENGTH: 1909			
		TYPE: DNA			
		ORGANISM: Human			
		US-09-949-016-5326			
		Query Match 23.0%; Score 389.2; DB 4; Length 1909;			
		Best Local Similarity 61.1%; Pred. No. 5.2e-81;			
		Matches 661; Conservative 0; Mismatches 398; Indels 23; Gaps 1;			
Qy	202	CATTGAGCCCGGCTGATGCTCTCTGCTGGGCTTGAAGTCCACACAGGCTGCA	261	665	CAATGATCTGTTGGCTAATGATGATCTTAACCAACAGGAGTGAATCACTGCACTTTCAA
Db	9	CCTCGAGCGCGCGGCAAGCTGCTCTGCGCGGAGGATCGACACACAGCATGCA	68	666	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	262	GATGCTGTCTCTGGGATGACACCGGCTGACGACTTCTGTGAGGACCAACAGGCGCT	321	667	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	69	GTTCCTCTTATGCTGCTGCGGTCATCGAGGACTTCCACCGAGGCAACCAAG	120	668	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	322	AGCAGGAGAACCAACCATGATCTTGACACAGCTCTTCCCGACACAGGCTGAGCTGCT	381	669	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	121	-----CATGATTATTGATTTTGGCAATTTCTCTCAGAAAGTGCTCCCTCAT	165	670	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	382	GGCGGCTTACGACGCTGCGGAGCGGCGGAGCGGCTGCTGCGACTACTCCCT	441	671	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	166	TGAGGCTTTCGAGACCTTGGGAGCTGGGCTGATCCAAAGTTTCTGCGACTACAGCT	225	672	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	442	GACGCTGGACATCACCGCATGGCATGAGAGCATCAAGAGGAGCTGAGGCGCTTGTCAA	501	673	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	226	TCATGTGGCAGTACGCTGGTGGAGTACCAGGTTAAAGAGAAATGAATCTTGTGCA	285	674	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	502	GGAGAGGGTGAATCTCTCTGCTTTCATGGGATCAAGGACCGGCTGAGGCTGAG	561	675	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	286	AGATAAGGTTTAACTCTTCAAGATGTTTATGGGCTATAAGATCTGTACATGCTGAC	345	676	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	562	CGACGCCAGATCTACGAGATCTTACGATCATCCGGGACCTGGGGCTTGGCCAGGT	621	677	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	346	AGACCTGGAGCTGTACGAGGCTTCTCTCGGTGAAGGAAATTTGAGCAATTTGCCAGGT	405	678	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	622	GACGCTGAGAACCGGGACATCTGTGAGGAGGAGCAGAGCGGTTGTGAGCTCGGCAT	681	679	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	406	CCATGGGAAATGGAGACTTAATTTGACAGGGGAGCAGAAAGATGTTGGCTTGGGAT	465	680	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	682	CACTGGCCCCAGGGGCACTGTCTACGCAACCGGAGGAGGTGAGGCTGAGGCGTGTGA	741	681	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	466	AACAGGCGCTTGGGGGCAACGAGCTGTGCGGCCAGAGGAGTGGAGGAGGAGGCAAGCT	525	682	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	742	CCGAGCTGTCACCATCGCAGCAGGCAAACTGCGCTCTAGCTACCAAGGTGATGAG	801	683	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	526	GAGAGGCAATCACCATGACCGAGCGTGAATCTGCTCTTACATTTGATGATGATGAG	585	684	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	802	CAAGGGGGCGCGGACCGCATCGCTCAGGGCCAGGCGCAGAGGGGTTGCTGTTTGGGA	861	685	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	586	CAAGCTGTCAGCTAAGGTGATAGCGGATGCAAGGAGAGATGGGAAGTGTCTATGGTA	645	686	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	862	GCCATCACCGCGAGCTGGGACCGAGCGGTTCACTACTGTGAGGAGAACTGGGCAAA	921	687	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	646	ACCCATGACGAGGAGCTTGGGACAGATGGCACTCACTACTGGAATAAAGATGGCAACA	705	688	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	922	GGCTGACGCTTGTGTCATATCACCTCTGTCACCCAGAGCCCAACGAGGAGGAGGAGG	981	689	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Db	706	TGAGGCCCAATGTCATGGGTCCACCTTTTGGGACAGAGCCCTTCAACACCGGACTTCT	765	690	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG
Qy	982	CACCTGCTTGTGTCCAGCGGGAGCTTCCAGGTGACAGGAGGCGGCGGCTGCACTTCC	1041	691	CACTGCCCCAGAGGCTGTGGCAAGCAAACTTCGGCTGATCCCCGAGGCAACCAACG

QY 439 CCTGCAGTGGACATCAACCCGATGGCATGAGAGCATCAAGGAGAGCTGGAGGCCCTGGT 498
Db 363 CTTCCAGTTTCCCATCACCTGGTGGAGCGAAACAGGTGGCTGAGAGAAATGGGCGAACTGGT 422
QY 499 CAAGGAGAGGGTGTGAATCTCTTCTGGTCTTCAATGSCATACAAAGGACCGGTGCCAGTG 558
Db 423 AGCCAGCATGGGGTGAACAGCTTCAAGCACTTCATGGCTTACAAGAAATGCAATCATGGC 482
QY 559 CAGCGACAGCCAGATGTACGAGATCTTTCAGCATCATCGGACCTGGGGGCTTTGGCCCA 618
Db 483 CGCCGACGACACCTGGTGGCCAGCTTCGAGCGCTGCTGCAACTGGGTGCCGTGCCAC 542
QY 619 GGTGCACTGTGAGAAACGGGAGCATGCTGGAGGAGAGAGAGCGGTGTGCTGGAGCTCGG 678
Db 543 CGTGCAATGCGGAGAACCGGCGAACTGGTGTACCACTTCGAGAAAAAACTGCTTGCCAGGG 602
QY 679 CATCACTGGCCCCGAGGGCCAGCTGCTCAGCCACCCCGAGGAGGTGGAGGCTGAGGCGGT 738
Db 603 CATGACCGGACGAGAGGCTCAACCCCTTTCGCGCCCTTCAAGTGAAGTGAAGCGGC 662
QY 739 GTACCGAGCTGTCAACCATCGCAAGCAGGCAAACTGCCCGCTGTACGTCAACCAAGGTGAT 798
Db 663 CAGCGCGCCCATCGTATTCGCGAAACCATTTGGTAGCGCGCTGTATGTGTGCACATTTC 722
QY 799 GAGCAAGGGGGCGGCCCGACGCTATCGCTCAGGCCAAGCGAGAGGGTGTGTGTTGG 858
Db 723 CAGCCGTGAAGCACTGATGAATCACTATGCAAGCGCCAAAGGGCCAGCGGTTTACGG 782
QY 859 GGAGCCCATCAACCGCAGGCTGGGCAACGAGCGGTTCACATCTGGAGCAAGAACTGGGC 918
Db 783 CGAAGTCTTGGCCCGGCCACCTGCTGTGGAGCAAGCGGTCTACCGTGACCGGACTGGGC 842
QY 919 CAAGGCTGACGCTTCTGCATCAACCCCTGTCAACCCAGAGACCCACACGCGCAGACCA 978
Db 843 CACTGCCGTGGCTAGCTGATGAGCCCGCGCTTCGCGCGGAGCACCCAGGAGCGCT 902
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QY 1039 CACCACCTGCCAGAGGCTGTGGGCAAGGCAACTTCGCGCTGATCCCGAGGGGCACCA 1098
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QY 1099 CGGCATTGAGGAGCGCATGTGATGTCTGGGAGAAATGTGTGGCTCTCGGAGAGTGA 1158
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QY 1159 CGAATGATGTTGTCGGGTGACAGTACAAATGTGCGCAAAATCTTCAATTTTACCC 1218
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Db 1140 ACGCAAGGGGCGCATCCGCGTGGTGTGCGAGCGCGACCTGCTGTGGGACCCGAGGG 1199
QY 1279 CACCAAGATCATCTCTGCCAAGACCCACAATCTGAAAGTGGAGTACAACTCTTCGAGGG 1338
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Db 1260 CCGCACTGTGCGGGGTCCCGAGCACACCATCAGCCAGGGCAAGGTGCTCTGGGCCGA 1319
QY 1399 CGGGAAGATG-TTTGTACCCCGGGGCGGGCGCTTCGTCCCTCGGAAAAATTCCTCG 1456
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 07:02:36 ; Search time 1081 Seconds
(without alignments)
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Perfect score: 1690
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues
Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1690	100.0	1690	9	US-09-986-632-9
2	1688.4	99.9	2741	20	US-10-723-860-5930
3	1686.8	99.8	2699	17	US-10-133-937-30
4	1686.8	99.8	2699	17	US-10-159-563-30
5	1686.8	99.8	2699	20	US-10-723-860-1486
6	1318.4	78.0	2352	21	US-10-498-788-60
7	980.2	58.0	2947	22	US-10-948-947A-48

8	965.4	57.1	1829	9	US-09-986-632-3	Sequence 3, Appli
9	965.4	57.1	4435	17	US-10-062-674-1971	Sequence 1971, Ap
10	963.8	57.0	4459	14	US-10-175-523-140	Sequence 140, App
11	963.8	57.0	4459	15	US-10-006-911-11	Sequence 11, Appli
12	963.8	57.0	4459	17	US-10-133-937-8	Sequence 8, Appli
13	963.8	57.0	4459	17	US-10-159-563-8	Sequence 8, Appli
14	963.8	57.0	4459	18	US-10-205-331-53	Sequence 53, Appli
15	963.8	57.0	4459	19	US-10-788-792-1	Sequence 1, Appli
16	963.8	57.0	4459	20	US-10-851-921-5	Sequence 5, Appli
17	963.8	57.0	4459	20	US-10-956-157-617	Sequence 617, Appli
18	963.8	57.0	4459	24	US-11-099-266-140	Sequence 140, App
19	963.8	57.0	5421	9	US-09-954-456-2178	Sequence 2178, Ap
20	963.8	57.0	5421	11	US-09-968-007A-432	Sequence 432, App
21	963.8	57.0	5421	15	US-10-171-581-178	Sequence 178, App
22	963.8	57.0	5421	15	US-10-006-911-3	Sequence 3, Appli
23	963.8	57.0	5421	19	US-10-776-827-66	Sequence 66, Appli
24	963.8	57.0	5421	19	US-10-775-169-34	Sequence 34, Appli
25	963.8	57.0	5421	20	US-10-807-308-1	Sequence 1, Appli
26	963.8	57.0	5421	21	US-10-843-641A-5205	Sequence 5205, Ap
27	963.8	57.0	5421	21	US-10-843-641A-5902	Sequence 6902, Ap
28	876.8	51.9	2869	15	US-10-084-817-351	Sequence 351, App
29	876.8	51.9	2928	17	US-10-133-937-33	Sequence 33, Appli
30	876.8	51.9	2928	17	US-10-159-563-33	Sequence 33, Appli
31	875.2	51.8	2842	9	US-09-986-632-7	Sequence 7, Appli
32	875.2	51.8	2842	9	US-09-736-457-1800	Sequence 1800, Ap
33	875.2	51.8	2842	9	US-09-902-941-1800	Sequence 1800, Ap
34	875.2	51.8	2842	9	US-09-849-626-1800	Sequence 1800, Ap
35	875.2	51.8	2842	14	US-10-017-754-1800	Sequence 1800, Ap
36	875.2	51.8	2842	16	US-10-113-872-1800	Sequence 1800, Ap
37	875.2	51.8	2842	17	US-10-283-017-1800	Sequence 1800, Ap
38	875.2	51.8	2842	21	US-10-852-335A-15	Sequence 15, Appli
39	873.4	51.7	1719	14	US-10-180-198-1	Sequence 1, Appli
40	850.6	50.3	5046	10	US-09-873-367C-102	Sequence 102, App
41	850.6	50.3	5046	21	US-10-843-641A-102	Sequence 102, App
42	850.6	50.3	5047	9	US-09-954-456-495	Sequence 495, App
43	850.6	50.3	5047	10	US-09-930-213-273	Sequence 273, App
44	850.6	50.3	5047	14	US-10-175-523-175	Sequence 175, App
45	850.6	50.3	5047	16	US-10-269-909-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1

US-09-986-632-9
; Sequence 9, Application US/09986632
; Patent No. US2002011994A1
; GENERAL INFORMATION:
; APPLICANT: AGUERA, Michelle
; TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention or
; CURRENT INVENTION: treatment of myelin disorders
; FILE REFERENCE: P06974US01/BAS
; CURRENT APPLICATION NUMBER: US/09/986,632
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/246,751
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-986-632-9

Query Match	100.0%	Score	1690	DB	9	Length	1690
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Db	1	GGCGCCCTTACCAGAGACCCCGAGGAGGAGTGCTTCCAGGCGCAAGAAAGCATCCC	60				
QY	61	CCGGATCAGGAGTGACCGCTTCTGTATCAGAGTGGGAGTCTGTGAATGACGACGATC	120				

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Qy	1201	AATCTTCAATTTT	TACCCCAAGGAAGGGCGAGTGGCTGTGGGCTCTGAACGCTGACCTGGT	1260
Db	1201	AATCTTCAATTTT	TACCAAGGAAGGGCGAGTGGCTGTGGGCTCTGAACGCTGACCTGGT	1260
Qy	1261	CATATGGAACCCCAAGGCCA	CCAAGATCATCTCTGCCAAGACCACAATCTGAACGTGGA	1320
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Qy	1321	GTACAAATCTTCGAGGAGTGA	GTGCTCGGGGAGCGCTCGCGTGGTCTAATAGTCAAGG	1380
Db	1321	GTACAAATCTTCGAGGAGTGA	GTGCTCGGGGAGCGCTCGCGTGGTCTAATAGTCAAGG	1380
Qy	1381	CCGAGTGGCGCTGGAGACGGGA	AGATGTTGTGCACCCGGGGGCGGGCGCTTCGTCCC	1440
Db	1381	CCGAGTGGCGCTGGAGACGGGA	AGATGTTGTGCACCCGGGGGCGGGCGCTTCGTCCC	1440
Qy	1441	TCGGMAAACAT	TCCCGACCTTGTCTACAAGAGATCAAGCTCGCAACAGGCTGGCGGA	1500
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Qy	1561	CAAGCCAGGAGTGGCGCT	CCGCGCGCGGTCTCTGCCAGGCAAGATCTCCGTGGCTCC	1620
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Qy	1621	TGTCGCAACTTACAT	CAGTCTGGGGTTCAGCCTATCTGGGTCTTCAGGCTGATGACACAT	1680
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RESULT 2
US-10-723-860-5930
; Sequence 5930, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5930
; LENGTH: 2741
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-5930

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	Best Local Similarity	99.9%	Pred. No. 0		
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Qy	61	CCGATCAGAGGTGACCGCTTCTGTATCAGAGTGGGAGGATCGTGAATGACACCAATC	120		
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Qy TGAGCTCCACAAAGGCTGACAGATGCTCTCTGGGATGACACCGGCTGACGACTTCTG 300
Db TGAGCTCCACAAAGGCTGACAGATGCTCTCTGGGATGACACCGGCTGACGACTTCTG 417
Qy TCAGGGCAACCAAGGCTGACAGATGCTCTCTGGGATGACACCGGCTGACGACTTCTG 360
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Qy CGACACGGGTGAGCTGCTGGGGCTTACGAGCACTGCGGAGCGGGGCGGACGCGC 420
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Qy GGTGGAGGCTGAGGCGGTGACCGAGCTGTCACCATCGCCAGGAGGAGGAGGAGGAGGAGGAG 780
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Qy GTAGCTCACCAGGTGATGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db GTAGCTCACCAGGTGATGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 957
Qy AGGGGTGCTGCTGTTGGGAGGCGGATCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db AGGGGTGCTGCTGTTGGGAGGCGGATCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1017
Qy CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077
Qy CCCACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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Qy 1681 CGCCCGACGC 1690
Db 1798 CGCCCGACGC 1807

RESULT 3

US-10-133-937-30
; Sequence 30, Application US/10133937
; Publication No. US20030207278A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 30
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-30

Query Match 99.8%; Score 1686.8; DB 17; Length 2699;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1688; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 CTTTTCAGCTGATGTCACGTCGGAAGATGGCTTTGATAAAACAAATCGGAGAAACCTTCAT 180

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QY 181 CQTCCCTGGGGGATCAAGACCAATGACCGCCCTGATGGTCTTCTCGTGGCGT 240
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QY 241 TGACGTCACACAAAGGCTGCAGATGCTGTCCTGGGCATGACACGGCTGACGACTTCG 300
Db 358 TGACGTCACACAAAGGCTGCAGATGCTGTCCTGGGCATGACACGGCTGACGACTTCG 417
QY 301 TCAGGGCACCAAGGACGCTAGCAGAGGAAACACCATGATCTTGACCAACGCTTCCC 360
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QY 361 CGACAGGGGTGAGCTGCTGGCGCTACAGAGCAGTGGCGGAGCGGGCGAGCAGCGC 420
Db 478 CGACAGGGGTGAGCTGCTGGCGCTACAGAGCAGTGGCGGAGCGGGCGAGCAGCGC 537
QY 421 GGCCTGCTGGACTACTCCCTGCACCTGGACATCACCCGATGGCATGAGGATCAAGGA 480
Db 538 GGCCTGCTGGACTACTCCCTGCACCTGGACATCACCCGATGGCATGAGGATCAAGGA 597
QY 481 GAGCTGAGGGCCCTGGTCAAGAGAGAGGTGTGAATCTCTCTCTGCTTTCATGGCATA 540
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Db 658 CAAGGACCGGTGCAATGACGACGACGACCAAGATGTACAGATCTTCAGCATATCCGGGA 717
QY 601 CTTGGGGGCTTGGCCCAAGTGCACCTGAGAACGGGACATCGTGGAGGAGGACGAA 660
Db 718 CTTGGGGGCTTGGCCCAAGTGCACCTGAGAACGGGACATCGTGGAGGAGGACGAA 777
QY 661 GCGGTTGCTGGAGCTCGGATCACTGGCCCGAGGCGCACGTGCTCAGCCACCCCGAGGA 720
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Db 838 GGTGAGGCTGAGCGGTGTACCGAGCTGTACCATGTGCAAGCAGGCAAACTGCCGCT 897
QY 781 GTACGTCACCAAGGTGATGAGCAAGGGGGCGGCGGACGATCGCTCAGGCGCAGCGAG 840
Db 898 GTACGTCACCAAGGTGATGAGCAAGGGGGCGGCGGACGATCGCTCAGGCGCAGCGAG 957
QY 841 AGGGGTGGTGTGTTGGGAGGCCATCACCGCAGCCTGGGCACCGAGGTTTCACTA 900
Db 958 AGGGGTGGTGTGTTGGGAGGCCATCACCGCAGCCTGGGCACCGAGGTTTCACTA 1017
QY 901 CTGGAGCAAGAACTGGGCCAAGGCTGAGCCTTGTGCATCACACCCCTGTCAACCCAGA 960
Db 1018 CTGGAGCAAGAACTGGGCCAAGGCGCAGCCTTGTGCATCACACCCCTGTCAACCCAGA 1077
QY 961 CCCACCAAGGACGACCACTTCACTCTGCTGTCTGTCAGGGGGGACCTTCAGGTGACGG 1020
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Db 1138 CAGCGGCCACTGCACTTCACTACCTGCCCAGAGAGGCTGTGGGCAAGGACAACTTCGCGCT 1197
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QY 1141 GGCCTCTGGGAGATGGAAGAGATGAGTTCTGTCGGGTGACACGATCAAAATCTGCCAA 1200
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QY 1201 AATCTTCAATTTTATCCAAAGGAGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGTT 1260

Db 1318 AATCTTCAATTTTATCCCAAGGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT 1377
QY 1261 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCAAGAGCCCAAACTCTGAACGTGA 1320
Db 1378 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCAAGAGCCCAAACTCTGAACGTGA 1437
QY 1321 GTACAAACATCTTTCAGGGAGTGGAGTGCAGGGAGCGCTGCGGTGTCATAAGTCAAGG 1380
Db 1438 GTACAAACATCTTTCAGGGAGTGGAGTGCAGGGAGCGCTGCGGTGTCATAAGTCAAGG 1497
QY 1381 CCGAGTGGCGCTTGGAGGACGGGAAGATTTTGTCAACCCCGGGGCGGGCGCTTCGTC 1440
Db 1498 CCGAGTGGCGCTTGGAGGACGGGAAGATTTTGTCAACCCCGGGGCGGGCGCTTCGTC 1557
QY 1441 TCGGAAAACATTTCCCGGACTTTGTCTACAGAGGATCAAAAGCTTCGCAACAGGTGGCGGA 1500
Db 1558 TCGGAAAACATTTCCCGGACTTTGTCTACAGAGGATCAAAAGCTTCGCAACAGGTGGCGGA 1617
QY 1501 GATTCACAGGTGTGCGCGGTGTATGACGGGCGCTTCACAGAGGTGATGGTGCCTGC 1560
Db 1618 GATTCACAGGTGTGCGCGGTGTATGACGGGCGCTTCACAGAGGTGATGGTGCCTGC 1677
QY 1561 CAAAGCAGGGAGTGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCTTC 1620
Db 1678 CAAAGCAGGGAGTGGCGCTTCGCGCGCGCTTCGCGCGCGCTTCGCGCGCGCTTC 1737
QY 1621 TGTGCGCAACCTACATCAGTTCGGGTTCAGCCTATCTGGGTCTCAGGCTGATGACCAT 1680
Db 1738 TGTGCGCAACCTACATCAGTTCGGGTTCAGCCTATCTGGGTCTCAGGCTGATGACCAT 1797
QY 1681 CGCCCGACGC 1690
Db 1798 CGCCCGACGC 1807

RESULT 4

US-10-159-563-30
; Sequence 30, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-30

Query Match 99.8%; Score 1686.8; DB 17; Length 2699;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1688; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCGCCCTTACCAAGAGACCCCGAGGAGGATGTCTTCCAGGGGCAAGAAAGCATCCC 60
Db 118 GCGCGCCCTTACCAAGAGACCCCGAGGAGGATGTCTTCCAGGGGCAAGAAAGCATCCC 177
QY 61 CCGGATCAAGGTGACCGGCTTCTGATCAGAGTGGAGGATCGTGAATGACGACGATC 120
Db 178 CCGGATCAAGGTGACCGGCTTCTGATCAGAGTGGAGGATCGTGAATGACGACGATC 237
QY 121 CTTTACGCTGATGTGTCAGTGGAGATGGCTTGTATATAAACAATCGGAGAAAACCTCAT 180

238 CTTTTCAGCTGATGTGCACGTGGAGATGCTTGATATAAAACAATCGGAGAAAACCTCAT 297
Db
181 CGTCCCTGGGGGCAATCAAGACCAATTGACCGCCACAGGCTGATGCTCTTCTGGTGGCGT 240
Qy
298 CGTCCCTGGGGGCAATCAAGACCAATTGACCGCCACAGGCTGATGCTCTTCTGGTGGCGT 357
Db
241 TGACGTCAACAAGGCTGAGATGCTCTGCTGGGCAATGACACCGGCTGACGACTTCTG 300
Qy
358 TGACGTCAACAAGGCTGAGATGCTCTGCTGGGCAATGACACCGGCTGACGACTTCTG 417
Db
301 TCAGGGCAACAGGCAAGGCTGAGGAGGAGAACACCATGATCTTGAACCAAGCTCTTCCC 360
Qy
418 TCAGGGCAACAGGCAAGGCTGAGGAGGAGAACACCATGATCTTGAACCAAGCTCTTCCC 477
Db
361 CGACACGGGTGTGAGCCTGTGCGGCTTACGAGCAGTGGCGGAGCGGGCGGACAGCGC 420
Qy
478 CGACACGGGTGTGAGCCTGTGCGGCTTACGAGCGGTGGCGGAGCGGGCGGACAGCGC 537
Db
421 GGCCTGTGCGACTATCTCCCTGACAGTGGACATCACCCGATGGCATGAGAGCATCAAGGA 480
Qy
538 GGCCTGTGCGACTATCTCCCTGACAGTGGACATCACCCGATGGCATGAGAGCATCAAGGA 597
Db
481 GGAAGTGGAGCGCTGTGCTGAGGAGAGGCTGTGAATCTCTGCTCTTCAATGGCATTA 540
Qy
598 GGAAGTGGAGCGCTGTGCTGAGGAGAGGCTGTGAATCTCTGCTCTTCAATGGCATTA 657
Db
541 CAAGGACCGGTGCGAGTGCAGCGACAGCAGATGTACGAGATCTTCAAGCATCATCCGGGA 600
Qy
658 CAAGGACCGGTGCGAGTGCAGCGACAGCAGATGTACGAGATCTTCAAGCATCATCCGGGA 717
Db
601 CTTGGGGGCTTGGCCAGGTGACCGTGTGAGAACCGGGACATCGTGGAGGAGGACAGAA 660
Qy
718 CTTGGGGGCTTGGCCAGGTGACCGTGTGAGAACCGGGACATCGTGGAGGAGGACAGAA 777
Db
661 GCGGTGCTGAGCTGGCATCACTGCGCCCGAGGGGCACTGCTGACGCCACCCCGAGGA 720
Qy
778 GCGGTGCTGAGCTGGCATCACTGCGCCCGAGGGGCACTGCTGACGCCACCCCGAGGA 837
Db
721 GGTGGAGGCTGAGCGGTGTACCGAGCTGTACCATCGCCCAAGCAGCAAACTGCCCGCT 780
Qy
838 GGTGGAGGCTGAGCGGTGTACCGAGCTGTACCATCGCCCAAGCAGCAAACTGCCCGCT 897
Db
781 GTACGTCAACAGGTGATGAGCAAGGGGGCGGCCAGCCATCGCTCAGGCCAAGCGCAG 840
Qy
898 GTACGTCAACAGGTGATGAGCAAGGGGGCGGCCAGCCATCGCTCAGGCCAAGCGCAG 957
Db
841 AGGGGTGCTGCTTTGGGAGGCGCCATCAACCGGAGCTGGGCAACCGGTTCACTTA 900
Qy
958 AGGGGTGCTGCTTTGGGAGGCGCCATCAACCGGAGCTGGGCAACCGGTTCACTTA 1017
Db
901 CTGGAGCAAGAACTGGGCGCAAGGCTGAGCGCTTCTGTCACATCACCCCTGTCAACCCAGA 960
Qy
1018 CTGGAGCAAGAACTGGGCGCAAGGCTGAGCGCTTCTGTCACATCACCCCTGTCAACCCAGA 1077
Db
961 CCCACCAAGGAGAGCAACCTCACTGCTTGTGTCAGGCGGAGCTTCCAGGTGACAGG 1020
Qy
1078 CCCACCAAGGAGAGCAACCTCACTGCTTGTGTCAGGCGGAGCTTCCAGGTGACAGG 1137
Db
1021 CAGCGGCCATGCACTTTCACATGCTGCTGTCAGGCGGAGCTTCCAGGTGACAGG 1080
Qy
1138 CAGCGGCCATGCACTTTCACATGCTGCTGTCAGGCGGAGCTTCCAGGTGACAGG 1197
Db
1081 GATCCCGAGGGGCAACCAAGGCTTGGAGGCGCATGCTGCTGCTGGGAGAAATGTGT 1140
Qy
1198 GATCCCGAGGGGCAACCAAGGCTTGGAGGCGCATGCTGCTGCTGGGAGAAATGTGT 1257
Db
1141 GGCCTCTGGGAAGATGAGCAAGGATGAGTTGCTGCGGCTGACCAAGTACAAATGCTGCCAA 1200
Qy
1258 GGCCTCTGGGAAGATGAGCAAGGATGAGTTGCTGCGGCTGACCAAGTACAAATGCTGCCAA 1317
Db
1201 AATCTTCAATTTTACCAAGGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT 1260
Qy
1318 AATCTTCAATTTTACCAAGGAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGT 1377
Db

1261 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCCAAGACCCCACAATCTGAACGTGGA 1320
Qy
1378 CATATGGAACCCCAAGGCCACCAAGATCATCTCTGCCAAGACCCCACAATCTGAACGTGGA 1437
Db
1321 GTACAAATCTTTCGAGGAGTGGAGTGCCTGGGAGAGCGCTTGGCGTGGTCAATAGTCAGGG 1380
Qy
1438 GTACAAATCTTTCGAGGAGTGGAGTGCCTGGGAGAGCGCTTGGCGTGGTCAATAGTCAGGG 1497
Db
1381 CCGAGTGGCGCTGAGGAGGAGGAGATGTTTGTACCCCGGGGGCGGCGCTTGGTCCC 1440
Qy
1498 CCGAGTGGCGCTGAGGAGGAGGAGATGTTTGTACCCCGGGGGCGGCGCTTGGTCCC 1557
Db
1441 TCGGAAAAATTCCTCCGAGCTTTTGTCTACAGAGAGATCAAAAGCTCGCAACAGGCTGGCGGA 1500
Qy
1558 TCGGAAAAATTCCTCCGAGCTTTTGTCTACAGAGAGATCAAAAGCTCGCAACAGGCTGGCGGA 1617
Db
1501 GATTCAGGTGTGCTGCTGGGCTGTATGACGGGCGCTTCCAGAGGTGATGCTGCTGC 1560
Qy
1618 GATTCAGGTGTGCTGCTGGGCTGTATGACGGGCGCTTCCAGAGGTGATGCTGCTGC 1677
Db
1561 CAAGCCAGGAGTGGCGCTCCGGCCGCGCTCCGGCCGCGCTCCGGCCGCGCTCCGGTCCC 1620
Qy
1678 CAAGCCAGGAGTGGCGCTCCGGCCGCGCTCCGGCCGCGCTCCGGCCGCGCTCCGGTCCC 1737
Db
1621 TGTGCGCAACCTACATCAGTCCGGGTTTCAAGCTTATCTGGGCTCTCAGGCTCATGACCAT 1680
Qy
1738 TGTGCGCAACCTACATCAGTCCGGGTTTCAAGCTTATCTGGGCTCTCAGGCTCATGACCAT 1797
Db
1681 CGCCCGACGC 1690
Qy
1798 CGCCCGACGC 1807
Db

RESULT 5

US-10-723-860-1486
; Sequence 1486, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05892.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1486
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1486

Query Match 99.8%; Score 1686.8; DB 20; Length 2699;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1688; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCGCGCCCTACCAAGAGACCCCAAGGAGCAGGATGCTCTTCCAGGGCAAGAAAGCATCCC 60
Db 118 GCGCGCCCTACCAAGAGACCCCAAGGAGCAGGATGCTCTTCCAGGGCAAGAAAGCATCCC 177
Qy 61 CCGGATCAGAGTGCACCGCTTCTGATCAGAGTGGGAGGATCGTGAATGACGACCAATC 120
Db 178 CCGGATCAGAGTGCACCGCTTCTGATCAGAGTGGGAGGATCGTGAATGACGACCAATC 237
Qy 121 CTTTACGCTGATGTCAGTGGAGAGTGGCTTGTGATAAAACAATCGGAGAAAACCTCAT 180
Db 238 CTTTACGCTGATGTCAGTGGAGAGTGGCTTGTGATAAAACAATCGGAGAAAACCTCAT 297

SOFTWARE: PERL Program
; SEQ ID NO 60
; LENGTH: 2352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506139CB1
US-10-498-788-60

Query Match 78.08; Score 1318.4; DB 21; Length 2352;

Best Local Similarity 89.3%; Pred. No. 0;
Matches 1509; Conservative 0; Mismatches 1; Indels 180; Gaps 1;

QY	1	GC	GC	CC	CT	AC	CA	GA	AG	CC	CC	CC	AG	AG	CA	GA	GT	CT	CC	AG	GG	CA	AG	AA	AG	CA	TCC	60	
DB	63	GC	GC	CC	CT	AC	CA	GA	AG	CC	CC	CC	AG	AG	CA	GA	GT	CT	CC	AG	GG	CA	AG	AA	AG	CA	TCC	122	
QY	61	CC	GG	AT	CA	CA	AG	TA	GC	CC	CT	TC	GA	T	CA	GA	GT	GG	AG	GA	T	CG	T	GA	AT	GA	CA	CG	120
DB	123	CC	GG	AT	CA	CA	AG	TA	GC	CC	CT	TC	GA	T	CA	GA	GT	GG	AG	GA	T	CG	T	GA	AT	GA	CA	CG	182
QY	121	CT	TT	TA	CG	CT	GA	T	GC	CA	CT	GG	AG	TA	GC	TT	GA	TA	AA	CA	AA	T	CG	GA	AA	AA	CA	CT	180
DB	183	CT	TT	TA	CG	CT	GA	T	GC	CA	CT	GG	AG	TA	GC	TT	GA	TA	AA	CA	AA	T	CG	GA	AA	AA	CA	CT	242
QY	181	CG	TC	CC	TC	GG	GG	CA	T	CA	AG	CA	TT	GA	CG	CC	CA	CG	CT	GA	T	GC	TT	CC	TC	GG	CG	240	
DB	243	CG	TC	CC	TC	GG	GG	CA	T	CA	AG	CA	TT	GA	CG	CC	CA	CG	CT	GA	T	GC	TT	CC	TC	GG	CG	302	
QY	241	TG	AC	GT	CC	CA	CA	AG	GT	CG	AG	T	GC	TC	GG	GG	CA	T	CA	CG	CG	TC	GA	CA	CT	TC	300		
DB	303	TG	AC	GT	CC	CA	CA	AG	GT	CG	AG	T	GC	TC	GG	GG	CA	T	CA	CG	CG	TC	GA	CA	CT	TC	362		
QY	301	TC	AG	GG	CA	CA	AG	CG	CG	TC	AG	CA	GA	GA	CA	CC	AC	CA	T	GC	TC	GA	CA	CG	TC	TC	360		
DB	363	TC	AG	GG	CA	CA	AG	CG	CG	TC	AG	CA	GA	GA	CA	CC	AC	CA	T	GC	TC	GA	CA	CG	TC	TC	422		
QY	361	CG	AC	CG	GT	GT	AG	CT	GT	CG	CG	CT	TA	CG	AG	CA	GT	GG	CG	AG	CG	CG	CA	CG	CG	CG	420		
DB	423	CG	AC	CG	GT	GT	AG	CT	GT	CG	CG	CT	TA	CG	AG	CA	GT	GG	CG	AG	CG	CG	CA	CG	CG	CG	482		
QY	421	GG	CT	GT	CG	CA	CT	TA	CT	CC	TC	GA	CA	CT	CA	CG	TA	TG	CA	TG	AG	CA	TC	AA	GG	CA	480		
DB	483	GG	CT	GT	CG	CA	CT	TA	CT	CC	TC	GA	CA	CT	CA	CG	TA	TG	CA	TG	AG	CA	TC	AA	GG	CA	542		
QY	481	GG	AG	CT	GG	AG	CC	CT	GT	CA	AG	GA	AG	GG	GT	GA	CT	CT	TC	TC	TC	TC	TC	TC	TC	TC	540		
DB	543	GG	AG	CT	GG	AG	CC	CT	GT	CA	AG	GA	AG	GG	GT	GA	CT	CT	TC	TC	TC	TC	TC	TC	TC	TC	602		
QY	541	CA	AG	GA	CC	GG	TC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	600		
DB	603	CA	AG	GA	CC	GG	TC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	GC	CA	662		
QY	601	CT	TC	GG	GG	CC	CT	TC	GG	CC	CA	GT	TC	GA	AG	CG	GA	CA	T	CG	T	GG	AG	CG	AG	CA	660		
DB	663	CT	TC	GG	GG	CC	CT	TC	GG	CC	CA	GT	TC	GA	AG	CG	GA	CA	T	CG	T	GG	AG	CG	AG	CA	722		
QY	661	CG	GT	TC	CG	AG	CT	CA	TC	GG	CC	CG	AG	CG	CA	CT	TC	GA	CG	CA	CC	CG	AG	CA	CG	AG	720		
DB	723	CG	GT	TC	CG	AG	CT	CA	TC	GG	CC	CG	AG	CG	CA	CT	TC	GA	CG	CA	CC	CG	AG	CA	CG	AG	782		
QY	721	GG	TC	GG	AG	CG	GT	T	AC	CG	AG	CT	TC	CA	CG	CG	CA	CG	CG	CA	CG	CG	CA	CG	CG	CG	780		
DB	783	GG	TC	GG	AG	CG	GT	T	AC	CG	AG	CT	TC	CA	CG	CG	CA	CG	CG	CA	CG	CG	CA	CG	CG	CG	842		
QY	781	GT	AC	GT	CA	CA	AG	GT	GA	T	GA	CG	GG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	840		
DB	843	GT	AC	GT	CA	CA	AG	GT	GA	T	GA	CG	GG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	902		
QY	841	AG	GG	GT	GG	TC	GT	TT	GG	AG	CG	CA	T	CA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	900		
DB	903	AG	GG	GT	GG	TC	GT	TT	GG	AG	CG	CA	T	CA	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	962		

RESULT 7

US-10-948-947A-48
; Sequence 48, Application US/10948947A
; Publication No. US20050130924A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Freier, Susan M.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Gaarde, William A.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: ANTISENSE INHIBITION VIA RNASE H-INDEPENDENT REDUCTION IN mRNA
; FILE REFERENCE: ISPH-0871
; CURRENT APPLICATION NUMBER: US/10/948, 947A

; CURRENT FILING DATE: 2004-09-24
 ; PRIOR APPLICATION NUMBER: 60/392,020
 ; PRIOR FILING DATE: 2002-06-26
 ; PRIOR APPLICATION NUMBER: 10/461,163
 ; PRIOR FILING DATE: 2003-06-13
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 2947
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (178)...(1896)
 ; OTHER INFORMATION: antisense oligonucleotide
 US-10-948-947A-48

Query Match 58.0%; Score 980.2; DB 22; Length 2947;
 Best Local Similarity 74.1%; Pred. No. 2.2e-266;
 Matches 1240; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

QY	18	CCCCAGGAGCAGGATGTCTTCCAGGCGCAAGAAAGCATCCCCCGGATCACGAGTGACC	77
DB	164	CGCCCCCGGAGAGATGTCTTATCAGGGGAAGAAATAATTCACGCGATCAGGCGATC	223
QY	78	GCCTTCGATCAGAGTGGGAGGATCGTGNATGACGACCGATCTCTTTAGCGCTGATGTC	137
DB	224	GTCTTCGATCAAAAGTGGCAAGATGTGAAATGATGACCGATCTCTTATGCGACATAT	283
QY	138	ACGTGGAAGATGCTTGATATAAAACAAATCGGAGAAACCTCATCGTCCCTGGGGGATCA	197
DB	284	ACATGGAGATGGTTGATCAAGCAATAGGAGAAACCTGATGTGCCAGAGGGGTGA	343
QY	198	AGACCATGTAGCGCCACGCGCTGATGGTCTTCTGGTGGCGTTGACGTCCACAAAGGC	257
DB	344	AGACCATCGAAGCCCACTCCAGAATGGTATCCCTGGAGGAAATGACGTGCACACTCGCT	403
QY	258	TGCAGATGCTGTCTGGGATGACACCGCTGACGACTTCTGTCAGGGGACCAAGGCGAG	317
DB	404	TCAGATGCGCAGACCGAGGAATACATCAGCTATGATCTTCTCCAGGGAAACCAAGGCGAG	463
QY	318	CGCTAGCAGAGGAACCAACCATGATCTTGACCAACGCTTCTCCCGACACAGGGTGTGAGCC	377
DB	464	CCCTGGCGGAGGAAACCAACCATGATCATCGACCATGTTGTTCTGAGCCCGGACAGCC	523
QY	378	TGCTGGCGGCTTACGACAGTGGCGGAGCGCGGACAGCGCGGCTGCTGCGACTACT	437
DB	524	TATTTGGCAGCCTTTTGATCAGTGGAGGAGTGGCGGACAGCAAGTCTCTGCTGTGACTATT	583
QY	438	CCCTGACAGTGGACATCACCCGATGGGATGAGAGCATCAAGGAGGAGCTGGAGCCCTGG	497
DB	584	CGCTGACGTTGGACATCACCGAGTGGCAAGGGCATCCAGGAGGAGATGGAAGCTCTGG	643
QY	498	TCAAGGAGAGGGTGTGAATCTCTCTGCTGTTCTATGGCATACAAGGACCGGTGCCAGT	557
DB	644	TGAAGGACCAAGGGGTAAATCTCTCTGCTGTACATGGGTTTCAAGATCGGTTCCAGC	703
QY	558	GCAGCGACGACAGATGTACGAGATCTTACGATCATTCGCGGACCTGGGGGCTTGGCCC	617
DB	704	TGACGGATTTCCAGATCTATGAAGTACTAGAGCGGTGATCCGGGATATTGGTGCCATAGCTC	763
QY	618	AGGTGACGCTGAGAACGGGACATCGTGGAGGAGGAGCAGAGCGGTCTCGAGCTCG	677
DB	764	AGTTCATGACAGAAATGGTGTGATCATCATTCAGAGGAAACAGCAGAGGATCCTGGATCTGG	823
QY	678	GCATCACTGCCCCGAGGGCCAGCTGCTCAGACCAACCCCGAGGAGGTGGAGGCTGAGCGCG	737
DB	824	GCATCACAGCCCCGAGGGGACAGCTGCTGAGCCCGGACAGAGAGGTTCGAGGCTGAAGCTG	883
QY	738	TGTACCGAGCTGTACCATCGCCACGACGCGCAACTGCCCGCTGTACGTCCACCAAGGTGA	797
DB	884	TGAACCGGCTCATCACCATTTGCCAATCAGACCAACTGCCCGCTGTATGTCCACCAAGGTGA	943

QY	798	TGAGCAAGGGGGCGCGCAGCGCATCGCTCAGGCCAAGCGCAGAGGGGTGGTCTGTTTG	857
DB	944	TGAGCAAGAGTGTCTGCTGAAGTCAATGCCCGCAGCAGCGAAGAGGAACCTGGGTATG	1003
QY	858	GGGAGCCCATCACCGCCAGCCTGGGACACGACGGTTTCACTACTCTGGAGCAAGAACTGGG	917
DB	1004	GTGAGCCCATCACTGCCAGCCTGGGACTGATGGCTCTCATTTATTGGAGCAAGAACTGGG	1063
QY	918	CCAAGGCTGACGCTTCTGTCATCATCCCCCTGTCTAACCCAGACCCCAACCGGAGACC	977
DB	1064	CCAAGGCGCTGCTTGTGCTCTCCACCTTTCAGCCCTTTCAGCCCGCAGCACTCCAGACT	1123
QY	978	ACCTACCTGCTTGTCTCCAGGGGACCTCCAGGTGACGACGCGCCCACTGCACCT	1037
DB	1124	TTCTCAACTCGTTGTCTCTGTGGAGACCTCCAGGTCACTGGAGTGGCCACTGTACCT	1183
QY	1038	TCACCACTGCCCAAGAGGCTGTGGGCAAGGACAACTTCCGCGCTGATCCCGGAGGACCA	1097
DB	1184	TCACCACTGCCCAAGAGGCTGTGGGCAAGGATAACTTCACTTGTATCCAGAGGACCA	1243
QY	1098	AGGCAATTCAGGAGCGCATGTGCTGTGGAGAAATGTGTGGCTCTGGGAAGATGG	1157
DB	1244	ATGGCACTGAGGAGCGGATGTCTGTCAATTTGGGATAAAGCTGTGGTCACTGGGAAGATGG	1303
QY	1158	ACGAGAACTGAGTTGTCGCGGTGACAGTACAAATGCTGCCAAATCTTCAATTTTACC	1217
DB	1304	ACGAGAACTGAGTTGTCGCGGTGACCTAGCACCAACGACGCCAAAGTCTTCAATCTTACC	1363
QY	1218	CAAGGAAGGGGCGAGTGGCTGTGGGCTGTGACGCTGACCTGGTTCATATGGAACCCCAAGG	1277
DB	1364	CACGGAAGGTCGTATCTCGTGGGATCTGACGACAGCTGGTGTGCTGGACCTTGACA	1423
QY	1278	CCACCAAGATCATCTCTGCCAAGACCAACAATCTGAACTGGAGTACAACTTTCGAGG	1337
DB	1424	GTGTGAAGACCATCTCTGCCAAGACGCAACAAGTCTTGGTACAACTTTTGAAG	1483
QY	1338	GAGTGGAGTGGCGGGAGCGCTGCGGTGTATAGTCAAGGCGCGAGTGGCGCTGGAGG	1397
DB	1484	GCATGGAGTGTGGGGCTCCCACTGGTGTATTCAGCCAGGGCAAGATTGCTTGGAGG	1543
QY	1398	ACGGGAAGATGTTTGTACCCCGGGGGCGGCTCTGCTCTCGTCCGGAACAACTTCCCGG	1457
DB	1544	ACGGCAGCTTGATGTTCACGGAAGGCTCAGGACGCTTACATCTCCCGGAAGCCCTTCCCTG	1603
QY	1458	ACTTTGTCTAAGAGGATCAAGCTCGCAACAGGCTGGGGAGATCCAGGTGTGCCCC	1517
DB	1604	ACTTTGTGTACAAACGATCAAGGCAAGGAGCAGGCTGGCTGAGCTGAGGGGGTCCCTC	1663
QY	1518	GTGGGCTGTATGACGGGCGGCTCCACGAGTGTGCTGCTGCCAAGCCAGGGAGTGGCG	1577
DB	1664	GTGGCTGTATGATGAGCCCGTATGCGAGGTGTCTGTGACGCCCAAGACGGTCACTCCGG	1723
QY	1578	CTCCGCGCGCGCTCTCTCCAGGCAAGATCTCTCGTGGCTCTCTGCGCAACTACATC	1637
DB	1724	CCTCATCAGTAAAGACATCCCTTCCCAAGCAGCAGCGCCACCTGTTGGAACCTGCACC	1783
QY	1638	AGTGGGGTTCAGCCTATCTGGGTCTCAGGCTGATGACACATCGCGCCGAGCC	1690
DB	1784	AGTCTGGTTTCAGCTTGTCTGGTGTCTCAGATTGACGACAACTTCCCGCGCGC	1836

RESULT 8
 US-09-986-632-3
 ; Sequence 3, Application US/09986632
 ; Patent No. US20020119944A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AGUERA, Michelle
 ; TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention or
 ; treatment of myelin disorders
 ; FILE OF INVENTION: P06974501/BAS
 ; CURRENT APPLICATION NUMBER: US/09/986,632
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: US 60/246,751

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; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-986-632-3

Query Match          57.1%; Score 965.4; DB 9; Length 1829;
Best Local Similarity 73.6%; Pred. No. 3.1e-262;
Matches 1230; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY 20 CCCAGAGCAGGATGCTCTTCCAGGGCAAGAAAGCATCCCCGGGATCAGAGTGACCGC 79
DB 60 CCCAGAGAGAGATGCTTATCAGGGGAGAGAAATATCCACGCATCAGAGCGATCGT 119
QY 80 CTTCTGATCAGAGTGGGAGATCGTGAATGACGACAGTCTTTTACGCTGATGTGCAC 139
DB 120 CTTCTGATCAAGGAGGTAAATTTGTTAATGATGACCGAGTCGTTCTATGCAGACATATAC 179
QY 140 GTGGAAGATGGCTTGTATATAAAACAAATCGAGAAACCTCATCTGCTGGGGGCATCAAG 199
DB 180 ATGGAAGATGGTTGATCAAGCAATAGGAGAAATCTGATTTGCCAGAGGAGTGAAAG 239
QY 200 ACCATTGACGCCCAACCGCTGATGTGCTCTTCTGTTGGCGGTTGACGCTGCCACACAAAGGCTG 259
DB 240 ACCATCGAGGCCCACTCCCGGATGTTGATCCCGGAGGAATTCACGTCACACTCGTTTTC 299
QY 260 CAGATGCTGCTCTGGGATGACACACCGGCTGACGACTTCTGTGTCAGGGGACCAAGGAGCG 319
DB 300 CAGATGCTGATCAGGGAATGACGCTGCTGTGATGATTTCTTCCAAAGGAACCAAGGGCGCC 359
QY 320 CTAGCAGGAGGAACCACTATGCTTTGGACCACTCTTCCCGACACGCGGTGAGCGCTG 379
DB 360 CTGGCTGGGGGAACCACTATGATGATGACCACTGTTGTTCTGAGCTTGGGACAGCGCTG 419
QY 380 CTGGCGGCTTAACAGCAGTGGCGGACCGGGCGGACAGCGCGCTCTGTCGCACTACTCC 439
DB 420 CTGCTGCTCTTACCACTGGAGGGAATGGCGCGACAGCAAGTCTCTGTGTGACTACTCT 479
QY 440 CTGCACTGGACATCAACCGATGGCATGAGAGCATCAAGAGAGCTGGAGGCGCTTGCTC 499
DB 480 CTGCATGTGACATCAGCGAGTGGCATTAAGGGGATCCAGGAGGAGATGGAAGCGCTTGTG 539
QY 500 AAGGAGAGGGTGTGAACTCTTCTGCTGCTTCTCATGSCATACAGAGACGCGTGCAGTGC 559
DB 540 AAGGATCAAGGGTAAATTTCTTCTGCTGTAATGCGCTTTCAAGATGCTTCCAGCTA 599
QY 560 AGCGACAGCCAGATGTACAGAGATCTTTCAGCATCATCCGGGACCTGGGGGCTTGGGCCAG 619
DB 600 ACGGATTCAGAGTTATGAAGTACTGAGTGTGATCCGGGATATTGGGCCATAGCCCAA 659
QY 620 GTGCACGTGAGAACGGGGACATCGTGGAGGAGGAGAGAGCGGTTGTGGAGCTCGGC 679
DB 660 GTCCACGCGCAAAATGCGACATCATTTGACAGGAGGAGCAGCAGAGGATCTTGGATCTGGGC 719
QY 680 ATCACTGGCCCCGAGGSCCAGCTGCTCAGCCACCCCGAGGAGGTGAGGCTGAGGCGGTG 739
DB 720 ATCAGGGGCCCCGAGGGACATGTGCTGAGCGGACCTGAGAGGTCCAGGCGCGAAGCCGTG 779
QY 740 TACCGAGCTGTCAACATCGCCAGCAGGCAAACTGCGCGCTGTACGTCACCAAGGTGATG 799
DB 780 AATCGTGCCATCAACATCGCCACACAGCAACCACTGCGCGCTGTATATCACCAGGTGATG 839
QY 800 AGCAAGGGGGCGGCCGACGCGCATCTGTGAGGCCAAGCGCAGAGGGGTGCTGTGTTTGGG 859
DB 840 AGCAAAAGCTCTGCTGAGGTCTATCGGCCAGGCAACGGAAGGAACCTGTGGTGTATGCG 899
QY 860 GAGCCCATCAACCGCCAGCTGGGCAACGAGCGGTTCACACTACTGGAGCAAGAACTGGGCC 919
DB 900 GAGCCCATCACTGCCAGCTGGGAACGAGCGGCTCCCTTACTTGGAGCAAGAACTGGGCC 959
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RESULT 9

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US-10-062-674-1971
; Sequence 1971, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaber, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1971
; LENGTH: 4435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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QY 920 AAGGCTGCGAGCCTTCTGTCAATCAACCCCTGTCAACCCAGAGCCCAACCGGAGACCCAC 979
DB 960 AAGGCTGCTGCGCTTTGTCTCACTCCCACTGAGCCCTGATCAACCACTTCCAGACTTT 1019
QY 980 CTCACCTGCTGCTGTCAGCGGGGACCTCCAGGTGACAGGAGCGGCCCACTGCACTTTC 1039
DB 1020 CTCACCTGCTGCTGTCAGCGGGGACCTCCAGGTGACAGGAGCGGCCCACTGCACTTTC 1079
QY 1040 ACCACTGCCAGAAAGGCTGTGGGCAAGGACAACTTCGCGCTGATCCCCGAGGGCACCAC 1099
DB 1080 AACACTGCCAGAGAGGCTGTAGGAAAGGACAACTTCACCTGATTCGGAGGGGACCAAT 1139
QY 1100 GGCATTGAGAGAGCGCATGTGATGCTGTGGGAGAAATGTGTGGCTCTTGGGAAAGTGGAC 1159
DB 1140 GGCATCTGAGAGCGCATGTCCGTCTCTGGGACAGGCTGTGTGCTCACTGGGAAAGTGGAT 1199
QY 1160 GAGATGAGTTCGTTCGGGTGACCAATGATGCTGCCAAATCTTCAATTTTACCCA 1219
DB 1200 GAGAACCACTTGTGTGGCTGTGACCAAGCAATGACAGCCAAAGTCTTCAACTTTACCCC 1259
QY 1220 AGGAAGGGCGAGTGGCTGTGGCTCTGACGCTGACCTGTCTATATGGAACCCCAAGGCC 1279
DB 1260 CGGAAGGGCGCATTTGCTGTGGATCCGATCCGACTGTGTCTGAGTACAACTTTGAAGGC 1319
QY 1280 ACCAAGATCATCTTCCCAAGACCCCAATCTGAACGTGGAGTACAACTTTTCGAGGGA 1339
DB 1320 GTTAAACCACTCTGCGCAAGACACACACAGCTCTCTCGAGTACAACTTTGAAGGC 1379
QY 1340 GTGGAGTGGGGGAGCGCTGCGGTGTCATAGTCAGGCGGAGTGGGCTGGAGGAC 1399
DB 1380 ATGGAGTGGCGGCTCCCACTGCTGTGGTCTCATCAGCAGGGGGAAGATTGTCTTGGAGGAC 1439
QY 1400 GCGAAGATGTTGTTCACCCCGGGGGCGCGCTGCTGCTCGGAAACCAATTTCCCGGAC 1459
DB 1440 GGCACCTGATGTCACCGAAGGCTCTGAGCGTACTATTTCCCGGAGGCGCTTCCCTGAT 1499
QY 1460 TTTGTCTACAGAGGATCAAGCTGCAACAGCTGCGGAGATCAACGCTGTGTCGCCCT 1519
DB 1500 TTTGTCTACAGCGTATCAAGGCAAGGAGCAGCTGCTGCTGAGTGAAGTGTCTGACCGCCCAAGACAGTCACTCCAGCC 1559
QY 1520 GGGCTGTATGAGGGGCGCTTCCAGAGGTGATGCTGCTGCCNAGCAGGGAGTGGGCT 1579
DB 1560 GGCCTGTATGAGCGGACCGCTGTGTGAAGTGTCTGTGACCGCCCAAGACAGTCACTCCAGCC 1619
QY 1580 CCGGCGCGCGCTCTGCGCCAGGCAAGATCTCCGTGCTCTGTGCGCAACCTTACATCAG 1639
DB 1620 TCTCGGCAAGAGCTCTCTGCGAAGCAGGAGGCGCCCACTGTGCGGAACCTGCAACAG 1679
QY 1640 TCGGGGTTTCAGGCTATCTGGGTCTCAGGCTGATGACCACTGCGCCCGAGCCG 1690
DB 1680 TCTGGATTTCAGTTTGTCTGCTCAGATTGATGACAACTTCCCGCGCGC 1730
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OTHER INFORMATION: Incyte ID No. US20040005559A1 371288.7
US-10-062-674-1971

Query Match 57.1%; Score 965.4; DB 17; Length 4435;
Best Local Similarity 73.6%; Pred. No. 3,7e-262;
Matches 1230; Conservative 0; Mismatches 441; Indels 0; Gaps 0;

QY	20	CCGAGGAGGAGTGTCTCCAGGCGAAGAAAGCATCCCGGATCACGAGTGACCGC	79
DB	229	CCGAGGAGAGATGTCTATCAGGGGGAAGAAAATATTCACGCATCAGAGCGATCGT	288
QY	80	CTTCTGATCAGAGGTGGGAGATCGTGAATGACGACAGTCTCTTTTACGCTGATGTGCAC	139
DB	289	CTTCTGATCAAGGAGGTAAATTTGTAATGATGACAGTCTCTTATGACAGATATAC	348
QY	140	GTGGAAGATGGCTTGATAAACAATTCGGGAAGAACTCTATCTCTCCCTGGGGGCATCAAG	199
DB	349	ATGGAAGATGGGTGATCAAGCAATATAGGAGAAATCTGATTTGTCCAGGAGGAGTGAAG	408
QY	200	ACCATTTGAGCCCAACGGCCTGATGTCTTCTGTGGGTGACGCTTGCACACAAAGCTG	259
DB	409	ACCATGAGGCCCACTCCCGATGGTGATCCCGAGGAATGACGCTCAACATCTCGTTTC	468
QY	260	CAGATGCTGTCTCTGGGCATGACACCGGCTGACGACTTCTGTCAAGGCGACCAAGGAGCG	319
DB	469	CAGATGCTGTATCAGGGAATGACGCTCTGTGATGATTTCTTCAAGGACCAAGGCGGCC	528
QY	320	CTAGCAGGAGGAACCAACCATGATCTTTGGACACGCTCTTCCCGACACGGGTGTGACCTG	379
DB	529	CTGGCTGGGGGAACCACTATGATCAATTGACCACTGTTCTCTGAGCTGGGACAAAGCTG	588
QY	380	CTGGCGGCTTACGAGCAGTGGGGGAGCGGGCGGACAGCGGCTCTGCTCGACTACTCC	439
DB	589	CTGCTGCTCTTACCAGTGGAGGAATGGGCGACAGCAAGTCTCTGCTGTGACTACTCT	648
QY	440	CTGCACTGTGACATCAACCGATGGCATGAGAGCATCAAGGAGAGCTGAGAGGCTCTGGTC	499
DB	649	CTGCTGTGGACATCAGCGAGTGGCATAGGGCATCCAGGAGAGATGGAAGGCTTTGTG	708
QY	500	AAGGAGAGGTGTAACTCTCTCTCTGTTTCTATGCGATACAAAGACCGGTGCCAGTGC	559
DB	709	AAGGATCAAGGGTAAATTTCTCTCTGTGTATGCTTCAAGATGCTTTCCAGCTA	768
QY	560	AGCGACAGCAGATGTACGAGATCTTCAGCATCATCGGACCTGGGGCTTTGGCCGAG	619
DB	769	ACGGATTGCCAGATTTATGAAGTACTGAGTGTATCCGGATATTTGGCGCCATAGGCCAA	828
QY	620	GTGCACTGTGAGAACGGGACATCTGTGGAGGAGGAGAGCGGTTGTCTGGAGCTCGGC	679
DB	829	GTCCACGCGAGAAATGGCGACATCTTGCAGAGGAGCAGAGGATCTCTGGATCTGGGC	888
QY	680	ATCACTGGCCCCGAGGCGCACGTCTCAGCCACCCGAGAGGTGAGGCTGAGGGCGGTG	739
DB	889	ATCAGCGGCCCCGAGGACATGTGCTGAGCGGACCTGAGGAGGTGAGGCGGAGCGGTG	948
QY	740	TACCGAGCTGTACCATGCGCAGCAGGCAAACTGCGCGTGTACGTCAACAGGTGATG	799
DB	949	AACTGTGCCATCACTACCATCGCAGCAACAGACCAATGCGCCGCTGTATATCAAGAGGTG	1008
QY	800	AGCAAGGGGGCGGCGGACGCTCTGCTCAGGCCAAGCGCAGAGGGGTGGTCTGTTTGGG	859
DB	1009	AGCAAAAGCTCTCTGAGGTCTATCGCCGAGGACGGAAGGMACTGTGTGTATGGC	1068
QY	860	GAGCCCATCAACCGCAGCTGGGACCGAGCGGTTTCACTACTGTGAGGAGAAAGACTGGGCC	919
DB	1069	GAGCCCATCACTGCCAGCTTGGGAAAGGAGCGGCTCCCATTTACTTGGAGCAAGAACTGGGCC	1128
QY	920	AAGGCTGACGCTTCTGATCACTACCCCTGTCAACCCAGCCCAACCGGAGGAGCCAC	979
DB	1129	AAGGCTGCTGCTTTGTCACTCTCCCACTTGGCCCTGATCCAACTCTCCAGACTTT	1188
QY	980	CTCACTCTGCTGTCTCAGCGGGGACCTTCAGGTGACAGGCGGCGCCACTGCACTTC	1039

DB	1189	CTCAACTCTTGTCTGTGTGGAGACCTCCAGGTCAAGGAGTCCCACTTTCACGCTTT	1248
QY	1040	ACCACCTGCCAGAGGCTGTGGGCAAGGACAACTTGGGCTGATCCCGAGGGCAGCAAC	1099
DB	1249	AACACTGCCAGAGGCTGTAGGAAAGGACAACTTCACTCTGATTCGAGGGGACCAAT	1308
QY	1100	GCATTTGAGGAGCGCATGTGATGGTCTGGGAGAAATGTGTGGCTCTCTGGGAAGATGGAC	1159
DB	1309	GGCATCTGAGGAGCGATGTCCGTCTCTGGGACAGGCTGTGTCTCTGGGAAGATGGAT	1368
QY	1160	GGAATGAGTTCGTCCGGTGACCAAGTCAAAATGTGCGCAAAATCTTCAATTTTACCCA	1219
DB	1369	GGAACCAAGTTTGTGGCTGTGACCAAGCAATTCAGCCAAAGTCTTCAACTTTACCCG	1428
QY	1220	AGGAAGGGCGAGTGGCTGTGGGCTCTGAGCTGACCTGCTCATATGGAACCCCAAGGC	1279
DB	1429	CGGAAGGGCGCATGTCTGTGGGATCCGATCCGACCTGCTCATCTTGGGACCCCGACG	1488
QY	1280	ACCAGATCATCTTGCACCAAGCAACCAATCTGAACGTGGAGTACAACTCTTCCGAGGGA	1339
DB	1489	GTTAAACCATCTTGCACCAAGCACACACAGCTCTCTGAGTACAACTCTTGAAGGC	1548
QY	1340	GTGGAGTCCGGGAGCGCTCCCGTGTCTATAAGTCAAGGCGGAGTGGCGCTTGGAGGAC	1399
DB	1549	ATGGAGTCCGGGCTCCCACTGTGTGTCTATCAGCCAGGGGAAAGTGTCTCTGGAGGAC	1608
QY	1400	GGGAGATGTTTGTACCCCGGGGGGGCGGCTTGTCTCTCGGAAACATTTCCCGGAC	1459
DB	1609	GGCACCTGCATGTCAACGAAGGCTCTGGACGCTACATTTCCCGGAAAGCTTCCCTGAT	1668
QY	1460	TTTGTCTCAAGAGGATCAAGCTCGCAACAGCTGGCGGAGATCCACGCTGTGCCCGCT	1519
DB	1669	TTTGTTCACAGGTATCAAGGCAAGGACAGGCTGGCTGAGCTGAGAGGGGTTCCTGCT	1728
QY	1520	GGGCTGTATGACGGGCGCTTCCACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1579
DB	1729	GGCTGTATGACGAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1788
QY	1580	CGGCGCGGCGCTTCCGCGGAGGATCTCGGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGT	1639
DB	1789	TCTCGGCAAGACGCTCTCTGCAAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1848
QY	1640	TGGGGTCTCAGCTATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1690
DB	1849	TCTGGATTGATTGT	1899

RESULT 10

US-10-175-523-140
; Sequence 140, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/10795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18

;; PRIOR APPLICATION NUMBER: US 60/361,834
;; PRIOR FILING DATE: 2002-03-04
;; NUMBER OF SEQ ID NOS: 197
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 140
;; LENGTH: 4459
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-175-523-140

Query Match 57.0%; Score 963.8; DB 14; Length 4459;
Best Local Similarity 73.5%; Pred. No. 1.1e-261;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

Qy	20	CCAGGAGCAGGATGTCCTTCCAGGGCAAGAAAGCATCCCGGATCACGAGTGACCGC	79
Db	263	CCAGGAGAGAGATGTCCTATCAGGGGAGAGAAATATCCAGCATCACGAGCGATCGT	322
Qy	80	CTTCTGATCAGAGTGGGAGGATCGTGAATGACGACGAGTCTTTTACGCTGATGTCAC	139
Db	323	CTTCTGATCAAGGAGGATGAATTTGTTAATGATGACGAGTCTTTATGCGACATATAC	382
Qy	140	GTGAGATGCTGTGATTAACAAATCGAGAAACCTCATCGTCCCTGGGGCATCAAG	199
Db	383	ATGGAAGATGGTTGATCAAGCAATAGAGAAATCTGATTTGCCAGGAGGTGAAG	442
Qy	200	ACCATGACGCCACCGCTGATGCTCTTCTGCTGGCGTTGACGTCCTCCACACAAAGCTG	259
Db	443	ACCATCGAGGCCACTCCCGGATGGTGTATCCCGGAGGAATTGACGTCCACATCGTTTC	502
Qy	260	CAGATGCTGTCTGGGATGACACCGGCTGACGATCTTGTGTCAGGGCAACAAGGACGC	319
Db	503	CAGATGCTGTATCAGGGAATGACGCTGTGCTGATGATTTCTTCCAAAGGAACCAAGCGGCC	562
Qy	320	CTAGCAGGAGAACCATCATGATCTTGACCACTCTTCCCGACACGAGTGTGAGCTG	379
Db	563	CTGGCTGGGGGAACCATATGATCATTTGACACGTTGTTCTTGAGCTGGGACAGCGCTG	622
Qy	380	CTGGCGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGCGCTCTCGACTACTCC	439
Db	623	CTCGCTGCTTTGACGAGTGGAGGGAATGGCCGACAGCAAGTCTCTGTGTACTCT	682
Qy	440	CTGCACTGACATCACCCGATGTCATGAGAGCATCAAGAGAGTGTGGAGGCTTGCTC	499
Db	683	CTGCACTGACATCAGCAGTGGCATTAAGGCAATCCAGGAGAGATGGAAGCGCTTGTG	742
Qy	500	AAGGAGAGGTGTGAATCTTCTCTGCTTCTGATGATGATGATGATGATGATGATGATG	559
Db	743	AAGGATCACGGGGTAAATCTTCTCTGCTGATGATGATGATGATGATGATGATGATG	802
Qy	560	AGCGACAGCAGATGTACGAGATCTTCAGCATCATCCGGACCTTGGGGGCTTGGCCAG	619
Db	803	ACGATTGCCAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	862
Qy	620	GTGCACTGAGAACGGGAGATCTGTGAGGAGGAGAGAGCGGTTGCTGAGCTCGGC	679
Db	863	GTCCACGAGAAATGGGACATCATTTGAGGAGGAGCAGCAGGATCTCTGATCTGGGC	922
Qy	680	ATCACTGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	739
Db	923	ATCACTGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	982
Qy	740	TACGAGCTGTGACCATCGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	799
Db	983	AATGTCCTCATCAATTCGCAACAGCAACATGCGCGCTGTATATCACCAAGGATG	1042
Qy	800	AGCAAGGGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	859
Db	1043	AGCAAAAGCTCTGCTGAGTCTATCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGG	1102
Qy	860	GAGCCCATCAACCGCAGCTGGGACCGAGCGTTTCACTACTGAGAGCAAGACTGGGCC	919
Db	1103	GAGCCCATCACTGCGAGCTTGGGAAACGAGCGGCTCCATTTACTGGAGCAAGAACTGGGCC	1162

Qy	920	AAGGCTGACGCTTGTGTCATCATCACCCCTGTCAACCCAGACCCACACGAGACCCAC	979
Db	1163	AAGGCTGCTGCTTTGTCACCTCCACACCTTGGCCCTGATCCAAACCATCTCCAGACTT	1222
Qy	980	CTCAGCTGCTTGTGTCAGCGGGGAGCTTCCAGGTGACAGGAGCGGACCTGACACTTC	1039
Db	1223	CTCACTCTCTTGTGTCAGTGTGAGAGCTTCCAGGTCAOGGGCAGTGGCCATTCACGCTT	1282
Qy	1040	ACCAGTCCCAAGAGGCTGTGGGCAAGGACAACTTGGCGCTGATCCCGAGGGGACCAAC	1099
Db	1283	AACACTGCCCAGAGGCTGTAGGAAAGGACAACTTCACTCTGATTCGGGAGGACCAAT	1342
Qy	1100	GGCATTTGAGAGGAGCGCATGTCGATGCTGTGGGAGAAATGTGTGGCTCTGGGAAAGTGAAC	1159
Db	1343	GGCACTGAGAGGCGGATGTCGTCATCTGGGACAGAGCTGTGTCTCACTGGGAAAGTGGAT	1402
Qy	1160	GAGAAATGTTCTGCGGGTGGACCATGACAAATGCTGCCAAATCTTCAATTTTACCCA	1219
Db	1403	GAGAACGAGTTGTGGCTGTGACCAACCAATGACAGCCAAAGTCTTCAACCTTTACCCC	1462
Qy	1220	AGGAAGGGGAGTGTGCTGTGGCTCTGACGCTGACCTGTGTCATATGGAACCCCAAGGCC	1279
Db	1463	CGGAAGGGCGCATTTGCTGTGGGATCGATGCGACCTGTGTCTATCTGGGACCCGACAGC	1522
Qy	1280	ACCAAGATCATCTCTGCCAAGACCCCAATCTGAACGTGGAGTACAACTTTTGGAGGA	1339
Db	1523	GTATAAACCATCTCTGCCAAGACACACACAGCTCTCTCGAGTACAACTTTTGAAGGC	1582
Qy	1340	GTGGAGTCCCGGAGCGCTGCTGTGTGTCATTAAGTCAGGCGGAGTGGCGCTGGAGGAC	1399
Db	1583	ATGGAGTCCCGCGCTCTCCCACTGTGTGTGTCATCAGCAGGCGGAGATTTGCTCTGGAGGAC	1642
Qy	1400	GGGAAGATGTTGCTCAACCCCGGGCGGCGCTGCTCTCCCTCGGAAACATTTCCCGGAC	1459
Db	1643	GGCACCTGTATGTCACCGAGGCTCTGGACGCTTACATTTCCCGGAGGCCCTTCCCTGAT	1702
Qy	1460	TTTGTCTTCAAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCCACGCTGTGCCCGCT	1519
Db	1703	TTTGTCTTCAAGGATCAAGCAAGGAGGAGGCTGGCTGAGCTGAGAGGGGTTCTCTCGT	1762
Qy	1520	GGGCTGTATGACGGGCGGCTTCCAGAGGTGATGGTCTGCCAAGCCAGGAGTGGCGCT	1579
Db	1763	GGGCTGTATGACGAGCTGTGTGTGAAGTGTCTGTGACGCGCCCAAGACAGTCACTCCAGCC	1822
Qy	1580	CGGCGCGGCGCTCTGCGCCAGGCAAGATCTCCGTGCTCTCTGCGCAACCTTACATCAG	1639
Db	1823	TCCTCGGCAAGAGCTCTCTGCAAGCAGGAGGCGCCCACTGTCCGGAACCTGACACAG	1882
Qy	1640	TCGGGGTTCAAGCTTATCTGGCTCTCAGGCTGATGACCACTCGCCCGGACGC	1690
Db	1883	TCGTGATTCAAGTTTGTCTGTGTCTCAGATTGATGACAACTTCCCGCGCGC	1933

RESULT 11

US-10-006-911-11
; Sequence 11, Application US/10006911
; Publication No. US20030125274A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF COLLAPLIN RESPONSE MEDIATOR PROTEIN 2 EXP
; FILE REFERENCE: RTS-0200
; CURRENT APPLICATION NUMBER: US/10/006,911
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 11
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-911-11

Query Match

57.0%; Score 963.8; DB 15; Length 4459;

Best Local Similarity 73.5%; Pred. No. 1.1e-261; Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;									
Qy	20	CCAGGAGCAGGATGTCCTTCAGGGCAAGAAAAGCATCCCCGGATCAGAGTGACCGC	79						
Db	263	CCAGGAGAGAGATGTCCTATACAGGGGAAGAAAATAATCCACGCATCAGAGCGATCGT	322						
Qy	80	CTTCTGATCAGAGGTGGAGATCGTGAATGACGACCAAGTCCTTTTACGCTGATGTGCAC	139						
Db	323	CTTCTGATCAAGAGGATGAATGTTGTTATGATGACCAAGTCGTTCTATGACACATATAC	382						
Qy	140	GTGGAAGATGGCTTGATAAAACAAATCGGAGAAAACCTCATCTCTCTGGGGCATCAAG	199						
Db	383	ATGGAAGATGGGTGATCAAGCAAAATAGAGAAAATCTGATTGTGCCAGGAGGTGAAG	442						
Qy	200	ACCATTTGACGCCACCGCTGATGTCCTTCCTGCTGCTGGCTTACGCTCCACACAAGGCTG	259						
Db	443	ACCATCGAGCCCACTCCCGGATGGTGATCCCGGAGGAATTGACGTCACATCTCGTTTC	502						
Qy	260	CAGATGCTCTCTGGGCATGACACCGGCTGACGACTTCTGTGAGGGCACCAAGGAGCG	319						
Db	503	CAGATGCTGATCAGGATGATGCTGTGCTGATGATTTCTTCAAGAACCAAGGGCGCC	562						
Qy	320	CTAGCAGGAGGAACCAATGATCTTTGGACCACTCTTCCCGACACAGGCTGTGACCTG	379						
Db	563	CTGGCTGGGGGAACCAATGATCTATTGACCACTGTTGTTCTGAGCCTGGGACAAGCCTG	622						
Qy	380	CTGGCGGCTTACAGCATGTGGCGAGCGGGCGGACAGCGCGCTCTGCTGCACTACTCC	439						
Db	623	CTCGCTGCTTTGACCACTGGAGGAATGGGGCGGACAGCAAGTCTCTGCTGACTACTCT	682						
Qy	440	CTCAGCTGACATCACCCGATGGCATGAGAGCATCAAGAGAGAGCTGGAGGCCCTGGTC	499						
Db	683	CTGCATGTGACATCAGCAGTGGCATTAAGGGCATCCAGGAGAGATGGAAGCGCTTGTG	742						
Qy	500	AAGGAGAAGGTTGAATCTCTTCTCTGCTTTCATGGCATAAAGACCGGTGCCAGTGC	559						
Db	743	AAGGATCAGGGGTAAATTCCTTCTCTGCTGTACATGGCTTTCAGAGATCGCTTCCAGCTA	802						
Qy	560	AGGCACAGCCAGATGTACGAGATCTTCAGCATCATCGGACCTCGGGGCTTGGGCCAG	619						
Db	803	ACGGATTGCCAGATTTATGAAGTACTGAGTGTGATCCGGGATATTGGCGCCATAGCCCAA	862						
Qy	620	GTCCAGCTGAGAACGGGGACATCTGTGGAGAGGAGCAGAGCGCTTGTGGAGCTCGGC	679						
Db	863	GTCCAGCAGAAAATGGCGACATCATTTGCGAGAGAGCAGCAGAGATCTTGGATCTGGGC	922						
Qy	680	ATCACTGGCCCCGAGGGCCACGTGCTCAGCCACCCGAGAGGTGGAGGCTGAGGGGGTG	739						
Db	923	ATCACGGGGCCCGAGGGACATGTGCTGAGCCGACCTGAGGAGGTTCGAGGCCGAAGCCGTG	982						
Qy	740	TACCGAGCTGTCAACATCGCCAAAGCAGGCAAACTGCCCGCTGTACGTACCAAGAGTGATG	799						
Db	983	AATCGTGCCATCACTACCGCAACACAGACCAACTGCCCGCTGTATATCACCAGGTGATG	1042						
Qy	800	AGCAAGGGGGCGCCGACCGCATCTGCTCAGGCCAAGCGCAGAGGGGTGCTGCTTTGGG	859						
Db	1043	AGCAAAAGCTCTGCTGAGGTGTCATCGCCCGAGCGACGGAAGGGAATGTGGTGTATGGC	1102						
Qy	860	GAGCCCATCAACCGCCAGCTGGGCAACCGAGCGTTTCACACTACTTGGAGCAAGAACTGGGCC	919						
Db	1103	GAGCCCATCACTGCCAGCTTGGGAACGAGCGGCTCCCATCTACTTGGAGCAAGAACTGGGCC	1162						
Qy	920	AAGGCTGACGCTTGTGTCATCAATCAACCCCTGTCAACCGACGCCACACGAGCAACAC	979						
Db	1163	AAGGCTGCTGCTTGTGCTACCTCCCACTCCCGCTTGAAGCCCTGATCCAACTCCAGCTTT	1222						
Qy	980	CTCACTGCTGCTGTGTCAGCGGGACCTCCAGGTGACAGCGCCCACTGCACTTC	1039						
Db	1223	CTCACTGCTGCTGTGCTGAGACCTCCAGGTCAAGGGAGTGGCCCACTTGCAGCTTT	1282						
Qy	1040	ACCACTGCCCAGAGGCTGTGGGCAAGGACAATCTGCGCTGATCCCCCGAGGGCAAC	1099						
Db	1283	AACACTGCCCAGAGGCTGTAGGAAAAGCAAACTTTCACCTGATTCGCGAGGGCACCAAT	1342						
Qy	1100	GCANTTGAAGAGCGCATGTCGATGCTCGGAGAAATGTGTGCCCTCTCGGAGATGGAC	1159						
Db	1343	GGCACTGAGGAGCGGATGTCCTGTCATCTGGGACAAAGGCTGTGTCTACTGGGAAGATGGAT	1402						
Qy	1160	GAGAATGATGCTGCTGCGGTGACCAAGTCAAAATGCTGCCAAAATCTTCAATTTTACCCCA	1219						
Db	1403	GAGAACCACTTGTGTGCTGTGACCAAGCAACCAATGACGCCAAGTCTTCAACTTTTACCCC	1462						
Qy	1220	AGGAAGGGCGAGTGGCTGTGGCTCTGACGCTGACCTGGTCATATGGAACCCCAAGGCC	1279						
Db	1463	CGAAAAGGGCGCATGCTGTGGGATCCGATCCGACCTGCTGCTATCTCTGGACCCCGCAGC	1522						
Qy	1280	ACCAAGATCATCTGTGCCAAGACCCACAATCTGAAAGTGTGAGGTACAAATCTTCGAGGGA	1339						
Db	1523	GTTAAACCATCTCTGCCAAGACACAAACAGCTCTCTCGAGTACAAATCTTTGAAGGC	1582						
Qy	1340	GTGGAGTCCGGGAGCGCTGCTGCTGCTGTCATAAGTCAAGGCGCGAGTGGCGTGGAGGAC	1399						
Db	1583	ATGGAGTCCGGCGCTCCCACTGCTGCTGCTATCAGCCAGGGGAGATTTGCTCTGGAGGAC	1642						
Qy	1400	GGGAAGATGTTGTTCACCCCGGGGGCGGCTTGTGCTCCCTCGGAAAACATTCGCGGAC	1459						
Db	1643	GGCACCTGCATGTCACCGAAGGCTCTGACGCTACATTCCTCCGGAAGCCCTTCCCTGAT	1702						
Qy	1460	TTTGTCTACAAGAGGATCAAGCTCGCAACAGCTGGCGGAGATCCACGGTGTGCCCTT	1519						
Db	1703	TTTGTCTACAAGCGTATCAAGGCAAGGACGAGCTGGCTGAGCTGAGAGGGGTTCCTCGT	1762						
Qy	1520	GGGCTGTATGACGGGCGCTGCCACAGGCTGATGCTGCTGCCAAGCCAGGAGTGGCGCT	1579						
Db	1763	GGCTGTATGACGACCTGTGTGTAAGTGTCTGTGACGCCCAAGACATCTACTCCAGCC	1822						
Qy	1580	CCGGCCCGCGCTCTGCCAGGCAAGATCTCCGCTCTCTGTGTGCGAACCTTACTATCAG	1639						
Db	1823	TCTCGGCAAGACGCTCTCTGCCAAGCAGCAGGCGCCACCTGTCCGGAACCTGCACACAG	1882						
Qy	1640	TCGGGGTTCAGCTATCTGGGTCTCAGGCTGATGACCAATCGCCGACGC	1690						
Db	1883	TCGGATTTCAGTTGTCTGCTGCTCAGATTGATGACAAATTCCTCCCGCGCCG	1933						
RESULT 12									
US-10-133-937-8									
; Sequence 8, Application US/10133937									
; Publication No. US20030207278A1									
; GENERAL INFORMATION:									
; APPLICANT: Khan, Javed									
; APPLICANT: Ringner, Markus									
; APPLICANT: Peterson, Carsten									
; APPLICANT: Meltzer, Paul									
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,									
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND									
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES									
; FILE REFERENCE: 11613.56US01									
; CURRENT APPLICATION NUMBER: US/10/133,937									
; NUMBER OF SEQ ID NOS: 99									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 8									
; LENGTH: 4459									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-133-937-8									
Query Match 57.0%; Score 963.8; DB 17; Length 4459;									
Best Local Similarity 73.5%; Pred. No. 1.1e-261;									
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;									
Qy	20	CCAGGAGCAGGATGTCCTTTCAGGGCAAGAAAAGCATCCCCGGATCAGAGTGACCGC	79						
Db	263	CCAGGAGAGAGATGTCCTATACAGGGGAAGAAAATAATCCACGCATCAGAGCGATCGT	322						

QY 80 CTTCTGATCAGAGTGGAGGATCGTGAATGACGACAGTCTTTTACGCTGTATGTCAC 139
DB 323 CTTCTGATCAAGGAGGTAAATTTGTTAATGATGACAGTCTTTTATGACATATAC 382
QY 140 GTGGAAGATGGCTTGATATAAACAATCGAGAAACCTCATCTGTCCTTGGGGGATCAAG 199
DB 383 ATGGAAGATGGTGTGATCAAGCAATAGGAAATCTGATTTGGCCAGGAGGTGAAG 442
QY 200 ACCATTACGCCACCGCTGATGCTCTTCTGCTGGCTTGACGTCCACACAGGCTG 259
DB 443 ACCATCGAGGCCACTCCGGATGGTATCCCCGAGGAATGACGTCCACACTCGCTTC 502
QY 260 CAGATGCTGTCTGCGCATGACACCGGCTGACGACTTCTGTCAAGGACACCAAGGACGCG 319
DB 503 CAGATGCTGTATCAGGGAATGACGCTCTGCTGATGATTTCTTCCAAGGAACCAAGGCGCC 562
QY 320 CTAGCAGAGGAACCAACATGATCTTGGACACAGTCTTCCCGACACAGGCTGTAGGCTG 379
DB 563 CTGCTGGGGGAACCACTATGATCAITGACACGCTGTTCTTGAGCCTGGGACAAAGCTG 622
QY 380 CTGCGGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGGCTGCTGCTGCTACTGCC 439
DB 623 CTGCTGCTTTGACCATGAGGGAATGGGCGACAGCAAGTCTCTGTGTGACTCTCT 682
QY 440 CTGCACTGGACATCACCCGATGGCATGAGAGCATCAAGGAGGAGCTGGAGGCTTGCTC 499
DB 683 CTGCACTGGACATCAGCGAGTGGCATAAAGGACATCAGGAGGAGATGGAAGCGCTTGTG 742
QY 500 AAGGAGAGGCTGTGAATCTTCTGCTGCTTCTATGACATCAAGGACCGGTGCAAGTGC 559
DB 743 AAGGATCAGCGGGTAAATCTTCTGCTGTATGATGCTTCAAGATCGCTTCCAGCTA 802
QY 560 AGCGACAGCAGATGTACAGATCTTCAAGCATCATCGGACCTGGGGCTTGGCCAG 619
DB 803 ACGATTGCCAGATTTATGAGTACTGAGTGTGATCCGGATATTTGGCGCCATAGCCAA 862
QY 620 GTGCACTGTGAAGACGGGACATCGTGGAGGAGGAGCAGAACGGCTTGTGAGCTCGGC 679
DB 863 GTCCACGACAGAAATGGGACATCATTTGACAGGAGGAGCAGAGGATCTTGGATCTGGGC 922
QY 680 ATCACTGGCCGAGGCGCACGCTGTGAGTCAAGCAGGAGGAGGAGGAGGAGGAGGAGG 739
DB 923 ATCAGCGGCGCGGAGGACATGTCTGAGCGGACCTGAGGAGGTCGAGGCGGAGCGGTG 982
QY 740 TACGAGCTGTCACTATCGCCACGACGAGCAAACTGCGGCTGTACGTCAACAGGTGATG 799
DB 983 AATGTCGCCATCACATCGCCAAACAGACCAACTGCGGCTGTATATCACCAAGGTGATG 1042
QY 800 AGCAAGGGGCGGCGGACGCTCGCTCAGGCGCAAGCGGAGGAGGAGGAGGAGGAGGAGG 859
DB 1043 AGCAAAAGCTCTGCTGAGTCTATCGCCGAGGACGGAAGGAACTGTGTGTATGGC 1102
QY 860 GAGCCCATACCGGACGCTGGGACCGAGCGGTTTCACTACTGAGCAAGAACTGGGCGC 919
DB 1103 GAGCCCATCACTGCGAGCTGGGAACGAGCGGCTCCCACTTACTGAGCAAGAACTGGGCGC 1162
QY 920 AAGCTGACGCTTCTGTCATATCACTACCCCTGTCAACGACCCCAACGAGGAGGAGGAGG 979
DB 1163 AAGGCTGCTGCTTGTGACATCTCCCACTTGGAGGCTGATCCAACTCCAGACTTT 1222
QY 980 CTCACTGCTGTCTGTCAGCGGAGCTCTCAGGTGACAGGAGGCGGCTGACCTTC 1039
DB 1223 CTCACTCTTGTCTGTGTGAGACTCTCAAGGTCAAGGAGGAGGAGGAGGAGGAGGAGG 1282
QY 1040 ACCATGCCCAGAGGCTGTGGGACAGGACAACTTCCGCTGTATCCCGAGGAGGAGGAGGAGG 1099
DB 1283 AACACTGCCCAGAGGCTGTAGGAAGGACAACTTCACTTCACTGAGGAGGAGGAGGAGGAGG 1342
QY 1100 GGCATTGAGAGGCGCATGTGATGCTGAGGAGGAAATGTTGGCTTCTGGAGGAGGAGGAGG 1159
DB 1343 GGCATGAGAGGCGGATGTCCGTCACTTGGGACAAAGGCTGTGCTGCTGAGGAGGAGGAGG 1402

QY 1160 GAGAAATGAGTTCCTCGGGTGACCAATGATGCTGCCAAATCTTCAATTTTACCCA 1219
DB 1403 GAGAACCAAGCTTTGCTGCTGTGACCAAGCAATGACGCAAGGCTTTCAACCTTTACCCC 1462
QY 1220 AGGAAGGGGAGTGTGCTGTGGCTCTGACGCTGACCTGTATATGGAACCCAGGCGC 1279
DB 1463 CGGAAGGGCGCATTCCTGTGGGATCCGATGCCGACTGTGTGAGGACCCGACAGC 1522
QY 1280 ACCAAGATCATCTCTGCCAAGACCCCAATCTGAAAGTGAGGTACAACTTTTCGAGGGA 1339
DB 1523 GTTAAACCAATCTCTGCCAAGACACACACAGCTCTCTCGAGTACAACTTTTGAAGGC 1582
QY 1340 GTGAGTGCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
DB 1583 ATGAGTGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1642
QY 1400 GGAAGATGTTTGTCAACCCCGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1459
DB 1643 GGCACCTGATGATCCAGGAGCTCTGAGCGCTATATTCCTCCGGAAGCCCTTCCCTGAT 1702
QY 1460 TTGTCTTACAGAGGATCAAGCTCGCAACAGGCTGCGGAGATCCACGGTGTGCCCGCT 1519
DB 1703 TTGTCTTACAGGATCAAGGCAAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1762
QY 1520 GGGCTGTATGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
DB 1763 GGGCTGTATGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1822
QY 1580 CGGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1639
DB 1823 TCCTCGGCGCAAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1882
QY 1640 TCGGGGTTTCAAGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1690
DB 1883 TCTGGATTCAGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1933

RESULT 13

US-10-159-563-8
; Sequence 8, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-8

Query Match 57.0%; Score 963.8; DB 17; Length 4459;
Best Local Similarity 73.5%; Pred. No. 1.1e-261;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

QY 20 CCAGAGGAGGAGTGTCTTCCAGGGGCAAGAAAGCATCCCGGATACAGAGTACCGC 79
DB 263 CCAGAGGAGAGATGTCTTATCAGGGGAGAGAAATATTCACGCTATCAGAGGAGTGT 322
QY 80 CTTCTGATCAGAGTGGAGGATCGTGAATGACGACGCTTCTTTACGCTGTATGTCAC 139
DB 323 CTTCTGATCAAGAGGAGTAAATTTGTTAATGATGACGAGTGTCTTATGACAGATATAC 382

QY 140 GTGGAAGATGGCTGTATATAAAATAATCGAGAAAACTCATCGTCCCTGGGGCATCAAG 199
DB 383 ATGGAAGATGGCTGTATATAAAATAATCGAGAAAACTCATCGTCCCTGGGGCATCAAG 442
QY 200 ACATTTGACGCCCAACCGGCTGATGGCTCTTCTGGTGGGCTTGAAGCTTCAACAAAGGCTG 259
DB 443 ACCATCGAGGCCCACTCCCGATGGTGTATCCCGAGGGAATTGACGCTCCACACTCGCTTTC 502
QY 260 CAGATCGCTGTCTGGGCTGACACCGGCTGACGATCTTCTGTGAGGGCCCAAGGCGAGCG 319
DB 503 CAGATCGCTGTATCAGGGAATGACGCTGTCTGTATGATTTCTTCCAGGAACCAAGCGGCC 562
QY 320 CTAGCAGGAGAAACCACTGATCTTTGGACACGCTCTTCCCGACACGCGGTGTGAGCCTG 379
DB 563 CTGGCTGGGGGAACCACTATGATCATTTGACCACTGTTTCTGTAGCCTGGGACCAAGCCTG 622
QY 380 CTGGCGCCTTACGACAGTGGCGGAGCGGGCGGAACGCGCGCCTGCTGCGACTACTCC 439
DB 623 CTGCTGCTTTCACCACTGGAGGAATGGGCCGACACGCAAGTCTGCTGTGACTACTCT 682
QY 440 CTGCACTGTGACATCAACCGATGGCATGAGAGCATCAAGGAGGCTTGGAGGCCCTGGTC 499
DB 683 CTGCACTGTGACATCAACCGATGGCATGAGAGCATCAAGGAGGCTTGGAGGCCCTGGTC 742
QY 500 AAGGAGAGGGGTGTGAATCTCTTCTGCTTCAATGGCATACAAAGGACCGGTGCCAGTGC 559
DB 743 AAGGATCAAGGGGTAAATTCCTTCTCTGCTGATGATGCTTCAAGATCGCTTCCAGCTA 802
QY 560 AGCGACAGCCAGATGTACGAGATCTTACGATCATCCGGGACCTGGGGGCTTTGGGCCAG 619
DB 803 ACGGATTCAGATTTATGAAGTACTGAGTGTGATCCGGGATATGGCGCCATAGGCCAA 862
QY 620 GTGCACTGTGAGAACCGGAGCATCTGTGGAGGAGCGAGCGGTGCTGGAGCTGGC 679
DB 863 GTCACGCGAGAAATGGCGACATCTTCGACAGAGGAGCGAGGATCTTGGATCTGGGC 922
QY 680 ATCACTGGGCCCCGAGGCCACGTGCTCAGCCACCCCGAGGAGGTGGAGGCTGAGGCGGTG 739
DB 923 ATCAAGGCCCCGAGGAGCATGTGCTGAGCCGACTTGGAGGAGGTGAGGCGCGAAGCGTG 982
QY 740 TACCGAGCTGTACCAATCGCCAAAGCGAGGAAATGCGCGCTGTACGCTACCAAGGATG 799
DB 983 AATCGTGCCATCACTACCAACCAAGAGCCAGCACTGCGCGCTGTATATCAAGGATG 1042
QY 800 AGCAAGGGGGCGGCGAGCCATCTGCTCAGGCCAAGCGGAGAGGGGTGTGCTGTTGG 859
DB 1043 AGCAAGGCTCTGCTGAGGTCATCGGCCCAAGCGGAGGAGGAACTGTGCTGTATGCG 1102
QY 860 GAGCCCATCAACCGCCTGGGCGACCGAGGTTTCACTACTTGGAGCAAGAACTGGGCC 919
DB 1103 GAGCCCATCACTGCGAGCTTGGGAACGAGCGGCTCCCATTTACTTGGAGCAAGAACTGGGCC 1162
QY 920 AAGGCTGACGCTTGTGTCATACACCCCTGTCAACCCAGACCCCAAGGAGGAGGAGGAG 979
DB 1163 AAGGCTGCTGCTTGTGCTACCTCCCAACCTTGGAGGCTGTATCCAACTTCCAGACTTT 1222
QY 980 CTCACTGCTGTGCTGTCAGCGGGGACCTTCAGGTGACGAGCGGCGCACTGCACTTC 1039
DB 1223 CTCACTGCTGTGCTGTCAGCGGGGACCTTCAGGTGACGAGCGGCGCACTTTCAGCTTT 1282
QY 1040 ACCACTGCCAGAGGCTGTGGGCAAGGACAACTTGGCGCTGTATCCCGAGGAGGAGGAGG 1099
DB 1283 AACACTGCCAGAGGCTGTGGGAAGGACAACTTCACTGATTCGGAGGAGGAGGAGGAG 1342
QY 1100 GGCAATTGAGAGCGCATGTGCTGTGGGAAGAAATGTGTGGCTCTTGGGAAGAGTGGAC 1159
DB 1343 GGCACTGAGAGGCGGATGTCCGTCACTTGGGACAAAGGCTTGGCTCACTGGGAAGAGTGGAT 1402
QY 1160 GAGCAATGATTTCTGCGGCTGACAGTACAAATGCTGCGCAAAATCTTCAATTTTACCCA 1219
DB 1403 GAGAAACGATTTGTGGCTGTGACAGCAACAAATGCGAGGCAAGGCTTCAACCTTTACCCC 1462
QY 1220 AGGAAGGGGCGAGTGGCTGTGGGCTCTGACGCTGACCTGGTCTATATGGAAACCCCAAGGCC 1279

DB 1463 CGGAAGGCGGCATGCTGTGGATCCGATCCGACCTGTCATCTGGGACCCCGACGC 1522
QY 1280 ACCAAGATCATCTCTGCGCAAGACCCCAATCTGAAGTGGAGTACAAATCTTCGAGGA 1339
DB 1523 GTTAAACCATCTCTGCCAAGACACAAACAGCTCTCTCGAGTACAAATCTTTGAAGC 1582
QY 1340 GTGGAGTCCGGGAGCGCTGCGGTGTGTCATAAGTTCAGGGCGGAGTGGCTGGAGGAC 1399
DB 1583 ATGGAGTCCGGCGGCTCCCACTGGTGGTTCATCAGCAGGGGAAGATTTCTCTGGAGGAC 1642
QY 1400 GGAAGATGTTTGTCAACCCCGGGCGGCGCTTCTGCTCCCTCGAAAAACATTTCCCGGAC 1459
DB 1643 GGCACCTCATGTTCACGAAGGCTCTGGAAGCTATATTCCTCCCGAAGCCCTTCCCTGAT 1702
QY 1460 TTTGTCTCAAGAGAGTCAAGCTGCGAACAGGCTGGCGGAGATCCACGGTGTGCCCGT 1519
DB 1703 TTTGTTTACAGCGTATCAAGGCAAGGAGCGCTGGCTGAGCTGAGAGGGGTTCCTCGT 1762
QY 1520 GGGCTGTATGACGGGCGGCTCCACGAGGTGATGCTGCTGCCAAGCCAGGGAGTGGCGCT 1579
DB 1763 GGCCTGTATGACGAGCTCTCTGCAAGCAGGAGGCGCCACCTGTCCGGAACCTGCACGAC 1822
QY 1580 CCGGCCCGGCGCTCTCTGCCAGCAAGATCTCCGTGCTCTCTGTGCGCAACCTTACATCAG 1639
DB 1823 TCTCGGCCAAGAGCTCTCTGCAAGCAGGAGGCGCCACCTGTCCGGAACCTGCACGAC 1882
QY 1640 TCGGGTTCAGGCTATCTGGGCTCAGGCTGATGACCAATCGCCCGAGC 1690
DB 1883 TCTGGATTTCAGTCTGTCTGTCTGCTCAGATTGATGCAAACTTCCCGCGCGC 1933

RESULT 14
US-10-205-331-53
; Sequence 53, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnoch, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Dihydropyrimidinase-related protein
US-10-205-331-53

Query Match 57.0%; Score 963.8; DB 18; Length 4459;
Best Local Similarity 73.5%; Pred. No. 1.1e-261;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

QY 20 CCCAGGAGCAGATGTCCTTCCAGGCGCAAGAAAGCATCCCGGATCAGGATGACCGC 79
DB 263 CCAGAGAGAGATGTCTTATCAGGGGAAGAAATATTTCCAGCATCAGGCGATCGT 322
QY 80 CTTCTCATCAGAGTGGGAGGATCGTGAATGACGACAGTCTCTTTTACGCTGATGTGCAC 139
DB 323 CTTCTCATCAGAGGAGTAAATTTTATGATGACCACTCGTCTTCTATGCAGACATATAC 382
QY 140 GTGGAAGATGGCTGTGATAAATAAATCGGAGAAAACTCATGCTCCCTGGGGGATCAAG 199
DB 383 ATGGAAGATGGGTTGATCAAGCAATAGGAGAAATCTGATTTGTGCCAGGAGTGAAG 442

200 QY ACCATTGACGCCACGGCGTGAATGGTCTTCTGGTGGCGTTGACGTCCACAAAGGCTG 259
443 Db ACCATCGAGGCCCACTCCCGGATGGTGAATCCCGGAGGAATGACGTCCCACTCGTTTC 502
260 QY CAGATGCTGTCTGCGGCGATGACACCGGCTGACGACTTCTGTGAGGCGACCAAGGCGAG 319
503 Db CAGATGCTGTATCAGGGAATGACGCTGCTGTATGATTTCTTCCAAAGGAACAAGGCGGCC 562
320 QY CTAGCAGAGGAACCAACATGATCTTGGACACAGCTCTTCCCGACAGCGGTGTGAGCCTG 379
563 Db CTGCTGGGGGACCACTATGATCAATTTGACCAAGTGTCTTCTGAGCCTGGGACAGGCTG 622
380 QY CTGGCGGCTTACGAGCAGTGGCGGAGCGGGCGGACAGCGCGCTCTGCTGCGACTACTCC 439
623 Db CTGCTGCTCTTACGAGTGGAGGAATGGGCGGACAGCAAGTCTCTGCTGTGACTACTCT 682
440 QY CTGCACGTGACATCACCCGATGACATGAGAGCATCAAGGAGGAGCTGGAGGCGCTGTGTC 499
683 Db CTGCATGTGACATCAGCGAGTGGCATTAAGGGCATCCAGGAGGAGATGGAAGCGCTGTG 742
500 QY AAGGAGAGGCTGTGAATCTCTCTGCTCTTCAATGACATACAGGAGCGGTGCGAGTGC 559
743 Db AAGGATCAGGGGTAAATCTCTCTGCTGTACATGCTTTCAAAGATCGCTTCCAGCTA 802
560 QY AGCGACAGCAGATGTACGAGATCTTCAGCATCATCCGGGACCTGGGGCTTTGGGCCAG 619
803 Db ACGGATTCGCCAGATTTATGAAGTACTGATGATGATCGCGGATATTGGCGCCATAGCCAA 862
620 QY GTGCACGCTGAGAACGGGACATCGTGGAGGAGGAGCAGAGCGGTTGCTGGAGCTCGGC 679
863 Db GTCCACGAGAAAATATGCGGACATCATTTGCGAGAGGAGCAGAGGATCTTGGATCTGGGC 922
680 QY ATCACTGGCCCGAGGCGCACGTCTCAGCACACCCCGAGGAGTGGAGGCTGAGGCGGTG 739
923 Db ATCAAGGCGCCCGAGGAGCATGTGCTGAGCGGACCTGAGAGGCTCGAGGCGGAGCGGTG 982
740 QY TACCGAGCTGTACCATCGCAAGCAGGCAAACTGCCGCTGTACGTGACCAAGAGGTGATG 799
983 Db AATCGTGCCATCACCATCGCCACCAAGCACCACTGCCCGCTGTATATCAACAAAGGTGATG 1042
800 QY AGCAAGGGGCGGCGGAGCGATCGCTCAGCGCCAGCGGAGAGGGGTGCTGTTTGGG 859
1043 Db AGCAAAAGCTCTGCTGAGGCTCATCGCCAGGCGACGGAAGAGGAACTGTGCTGTATGCG 1102
860 QY GAGCCCATCACCGCTGCGGCGACGCGGTTTCACTACTGAGCAGAGAACTGGGCC 919
1103 Db GAGCCCATCATCGGCTTGGGAGCGGAGCGGCTCCCATTTACTGGAGCAAGAACTGGGCC 1162
920 QY AAGGCTGACGCTTGTGTCACATCACCCCTGTGCAACCCAGACCCACACCGGCGAGCAC 979
1163 Db AAGGCTGCTGCTTGTGTCACCTCCCACTTGGAGCTTGTATCCACCACTCCAGACTTT 1222
980 QY CTCACTGCTGTGCTCCAGGGGACCTCAGGTGACAGGCGGCGCCACTGCGACCTTC 1039
1223 Db CTCACTCTCTGTGCTCTGTGAGACCTCAGGTGACGCGGCGAGTGCCTTGCAGCGTTT 1282
1040 QY ACCACTGCCAGAGGCTGTGGGCAAGGACAACTTGGCGGTGATCCCGAGGCGACCAAC 1099
1283 Db AACACTGCCAGAGGCTGTAGGAAGGACAACTTCACTTCCCTGATTCGGAGGGGACCAAT 1342
1100 QY GGCAATTGAGAGGCGCATGTGATGCTGGGAGAAATGTGTGGCTCTCGGGAAGATGGAC 1159
1343 Db GGCATCTGAGAGCGGATGTCGTCATCTGGGACAGGCTGTGCTCACTGGGAGATGGAT 1402
1160 QY GAGATGAGTGTGTCGGGTGACCAAGTAAATGCTGCCAAAATCTTCAATTTTACCCA 1219
1403 Db GAGAACCAAGTGTGTGGCTGTGACCAAGCAACCAATGACGCAAAAGTCTTCAACCTTTACCCC 1462
1220 QY AGNAGGGGAGTGGCTGTGGCTCTGACGCTGACCTGCTCATATGGAAACCCCAAGGCC 1279
1463 Db CGGAAAGGCGCATGTGCTGGGATCCGATGCGGACCTGCTCATCTGGGACCCCGCAGC 1522

1280 QY ACCAAGATCATCTCTGCCAAGACCCACAAATCTGAACGTGAGTACAAATCTTTCGAGGGA 1339
1523 Db GTTAAAAACCATCTCTGCCAAGACACACACAGCTCTCTCGAGTACAAATCTTTCGAGGC 1582
1340 QY GTGGAGTCCCGGAGCGCTGCTGATCAAGTCAAGGCGAGTGGCGCTGGAGGAC 1399
1583 Db ATGGAGTCCCGGCTCCCACTGCTGCTGATCAAGCAGGAGGAGATTTCTTGGAGGAC 1642
1400 QY GGGAAGATGTTTCTACCCCGGGGCGGCGCTTCTCTCGGAAAAATTTCCCGGAC 1459
1643 Db GGCACCTGCTATCCACCGAAGCTCTGAGAGCTTACATTTCCCGGAAGCTTTCCTGAT 1702
1460 QY TTTGTCTACAGAGGATCAAGCTCGCAACAGGCTGGCGGAGATCAACGCTGTCGCCCT 1519
1703 Db TTTGTCTTACAGGCTTCAAGGCAAGGAGCAGGCTGGCTGAGCTGAGAGGCTTCTCTGT 1762
1520 QY GGCTGTATGACGCGGCGCTCCACAGGCTGATGCTGCTGCCAAGCCAGGAGTGGCGCT 1579
1763 Db GGCTGTATGACGAGCTGTGTGAGTGTCTGTGAGCCCAAGACAGTCACTTCCAGCC 1822
1580 QY CCGGCGGCGCTCTCTGCCAGGCAAGATCTCGCTGCTCTCTGCGCAACCTTACATCAG 1639
1823 Db TCCTCGGCCAAGAGCTCTCTGCCAAGCAGGCGGCCACCTTCTCGGAACCTGCACAG 1882
1640 QY TCGGGGTTCAAGCTTATCTGCTCTCAGGCTGATGACATATCGCCCGACGC 1690
1883 Db TCTGATTCAGTTTGTCTGCTGCTCAGATTCAGATTCAGCAACATTTCCCGCGCGC 1933

RESULT 15

US-10-788-792-1
; Sequence 1, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-792-1

Query Match 57.0%; Score 963.8; DB 19; Length 4459;
Best Local Similarity 73.5%; Pred. No. 1.1e-261;
Matches 1229; Conservative 0; Mismatches 442; Indels 0; Gaps 0;

20 CCAGAGCAGGAGTGTCTTCCAGGCAAGAAAGCATCCCGGATCAGGAGTGCAGC 79
263 CCAGAGGAGAGTGTCTTATCAGGGGAGAGAAATATTCACGCTACAGAGGATCGT 322
80 CTTCTGATCAGAGGTGGGAGGATCGTGAATGACGACAGTCTTTTACGCTGATGTGAC 139
323 CTTCTGATCAAAGGAGGTAAATTTTAATGATGACGACGCTGCTTATGACAGATATAC 382
140 GTGGAAGATGGCTGTGATAAACAATCGGAGAAACCTCATCTCTCGGGGATCAAG 199
383 ATGGAAGATGGGTGTGATCAAGCAATAGGAGAAATCTGATTTGCCAGGAGGATGA 442
200 ACCATTGACGCCCAACCGCTGATGCTCTCTGCTGGGCTTGCAGCTCCACACAAGGCTG 259
443 ACCATCGAGGCCCACTCCCGGATGGTGTATCCCGGAGGATTCAGCTTCCACTCTGTTTC 502
260 CAGATGCTGTCTCGGCGATGACACCGGCTGACGACTTCTGTGAGGCGACCAAGGCGG 319

Db 503 CAGATGCTGATCAGGAAATGACGTCTGCTGATGATTTCTTCAAGAAACCAAGCGGCC 562
Qy 320 CTAGCAGGAGAACCACTGATCTTGGACCAAGTCTTCCCGACACGGGTGTGACCTTG 379
Db 563 CTGGCTGGGGGAAACCACTATGATCATTTGACCAAGTCTTCTGAGCTGGGACACGCTTG 622
Qy 380 CTGGCGGCTTACGAGCAGTGGCGGAGCGGCGGACAGCGCGCTGCTGCGACTACTCC 439
Db 623 CTGCTGCTTTGACAGTGGAGGGAAATGGGCCGACAGCAAGTCTCTGCTGTGACTACTCT 682
Qy 440 CTGCACTGGACATCAACCCGATGGCATGAGAGCATCAAGAGAGAGCTGGAGGCCCTGGTC 499
Db 683 CTGCATGTGGACATCAGCAGTGGCATAGGGCATCCAGGAGAGATGGAAGCGCTTGTG 742
Qy 500 AAGGAGAGGGTGTGAATCTCTCTGCTGCTTCAATGGCATAAAGAACCGGTGCGATGC 559
Db 743 AAGGATCAGCGGGTAAATTCCTCTCTGCTGTACATGGCTTCAAGATCGCTTCCAGCTA 802
Qy 560 AGCGACAGCCAGATGTACGAGATCTTCAGCATCATCCGGACCTGGGGCTTTGGCCAG 619
Db 803 ACGGATTGCCAGATTTATGAGTACTGAGTGTGATTCGGGATATTTGGCCCATAGCCCAA 862
Qy 620 GTGACGCTGAGAACCGGGACATCGTGGAGGAGAGCAGAACGGTTGCTGGAGCTCGGC 679
Db 863 GTCCACGACAGAAATGGCGACATCATTTGCAGAGAGAGCAGCAGAGGATCCTGGATCTGGGC 922
Qy 680 ATCACTGGCCCCGAGGCCACGTGCTCAGCCACCCCGAGGAGGTGAGGCTGAGGCGGTG 739
Db 923 ATCACGGGCCCCGAGGGACATGTGCTGAGCCGACCTGAGGAGGTGAGGCCCCGAAGCCGTG 982
Qy 740 TACCGAGCTGTCAACATCGCAAGCAGGCAAACTGCGCGCTGTACGTACCAAGAGGTGATG 799
Db 983 AATCGTGCCATCAACATCGCAACAGCAGCAGTCCGCTGTATATACCAAGGTGATG 1042
Qy 800 AGCAAGGGGGCGCCGACGCGCATCGCTCAGGCCAAGCGCAGAGGGGTGCTGTTTGGG 859
Db 1043 AGCAAAAGCTCTGCTGAGGTCTATCGCCACGACCGGAAGAGAACTGTGGTGTATGGC 1102
Qy 860 GAGCCCATCAACCGCAGCTTGGGACCGGAGGTTCACTACTGGAGCAAGAACTGGGCC 919
Db 1103 GAGCCCATCACTGCCAGCTTGGGAAACGGACGGCTCCCATTTACTGGAGCAAGAACTGGGCC 1162
Qy 920 AAGGCTGCAGCCTTGTGTCATCAACCCCTGTCAACCCAGACCCACCGCAGCACAC 979
Db 1163 AAGGCTGTGCTTGTGCTACTCCACCCCTTGAGCCCTGATCCACCACTCCAGACTTT 1222
Qy 980 CTCACTGCTGTGCTCAGCGGGGACCTCCAGGTGACAGCGAGCGCCACTGCACTTC 1039
Db 1223 CTCAACTCTGCTGTGCTGTGAGAGACCTCCAGGTCAAGGGCAGTGGCCCATTCAGGTTT 1282
Qy 1040 ACCACTGCCAGAGGCTGTGGCAGGACAACTTGGCGTGTATCCCGAGGGGACCAAC 1099
Db 1283 AACACTGCCAGAGGCTGTAGAAAGGACAACTTCAACCCTGATTCGGAGGGGACCAAT 1342
Qy 1100 GGCATTGAGGAGCGCATGTGATGTCTGGAGAAATGTGTGCTCTGGGAAAGATGGAC 1159
Db 1343 GGCATGTAGAGAGCGGATGTCCGTCACTGAGGACAGGCTGTGTGCTGAGGAGATGGAT 1402
Qy 1160 GAGAATGAGTTGCTGCGGTGTGACAGTACAAATGTCTGCCAAATCTTCAAATTTTACCCA 1219
Db 1403 GAGAACCAAGTTTGTGGCTGTGACAGCACCAATGACAGCAAAAGTCTTCAACCTTTACCCC 1462
Qy 1220 AGGAAGGGGCGAGTGGCTGTGGCTGTGACGCTGACCTGCTCATATGGAAACCCCAAGGCC 1279
Db 1463 CGAAAGGGCGCATTTGCTGTGGATCCGATGCGGACCTGCTCATCTGGGACCCCGACAGC 1522
Qy 1280 ACCAAGATCATCTGCAAGAGCCCAAACTGAAAGTGGAGTACAACTCTTTCGAGGGA 1339
Db 1523 GTTAAACCATCTCTGCCAGAGACACACAGCTCTCTCAGGTACAACTCTTTGAGGC 1582
Qy 1340 GTGAGTGGCGGGAGCGCTGCGGTGTTATAGTCAGGGCCGAGTGGCGCTGGAGGAC 1399
Db 1583 ATGGAAGTGGCGGCTCCCCACTGGTGGTTCATCAGCCAGGGGAAAGATTGTCTCTGGAGGAC 1642

Qy 1400 GGGAAGATGTTTTGTCAACCCCGGGGCGGCGCTTCTGTCCTCGGAAAAACATTCCCGGAC 1459
Db 1643 GGACCCCTGCATGTCAACCGAAGGCTCTGACACGTTACATTCCCGGAAAGCCCTTCCCTGAT 1702
Qy 1460 TTTGTCTACAAGAGGATCAAAAGCTCGCAACAGGCTGGCGGAGATCCACGTTGTGCCCGCT 1519
Db 1703 TTTGTTTACAAGCGTATCAAGGCAAGGAGCAGGCTGGCTGAGCTGAGAGGGGTTCCTCGT 1762
Qy 1520 GGGCTGTATGACGGGCGCTGCCACAGGTTGATGGTGCCTGCCAAGCCAGGGAGTGGCGCT 1579
Db 1763 GGCCTGTATGACGGGACCTGTGTGTAAGTGTCTGTGACGCCCAAGACAGTCACTCCAGCC 1822
Qy 1580 CCGGCCCGCGCTTCTGCCCCAGGCAAGATCTCGGTGCTCTGTCGCAACCTACATCAG 1639
Db 1823 TCTCGGCCCAAGACGTTCTCTGCAAGCAGGAGGCCACCTGTCCGGAACTTGCACCCAG 1882
Qy 1640 TCGGGGTTTCAGGCTATCTGGGTTCTCAGGCTGATGACCAATCGCCCGACGC 1690
Db 1883 TCTGGATTCAAGTTTGTCTGTGCTCAGATTGATGACAAACATTCCCGCGCGC 1933

Search completed: September 24, 2005, 16:52:25
Job time : 1087 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2005, 14:19:36 ; Search time 1390 Seconds
(without alignments)
210.726 Million cell updates/sec

Title: US-09-367-496C-8

Perfect score: 2982

Sequence: 1 MSFGKKSIPRITSDLLR.....RTAQKIMAPPGRSNTISLS 572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
' score greater than or equal to the score of the result being printed,
' and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2978	99.9	572	1 DPY4 HUMAN	O14531 homo sapien
2	2824	94.7	572	1 DPY4 MOUSE	O35098 mus musculu
3	2795	93.7	564	1 DPY4 RAT	O62951 rattus norv
4	2519	84.5	574	2 Q9DJZ6	O9dd26 gallus gall
5	2488	83.4	650	2 Q71SG0	O71890 gallus gall
6	2441.5	81.9	668	2 Q7ZTP7	O7ztp7 xenopus lae
7	2368	79.4	572	1 DPY2 CHICK	O90635 gallus gall
8	2361	79.2	572	2 Q71SG1	O71891 gallus gall
9	2353	78.9	572	1 DPY2 BOVIN	O02675 bos taurus
10	2349	78.8	572	1 DPY2 RAT	P47942 rattus norv
11	2349	78.8	572	2 Q6P5D0	O6p5d0 mus musculu
12	2345	78.6	572	1 DPY2 HUMAN	O16555 homo sapien
13	2331	78.2	572	1 DPY2 MOUSE	O08553 mus musculu
14	2315	77.6	676	2 Q71SG2	O71892 gallus gall
15	2276	76.3	573	2 Q6PB02	O6pb02 xenopus lae
16	2215.5	74.3	571	2 Q6GL72	O6gl72 xenopus tro
17	2209.5	74.1	571	2 Q640K6	O640k6 xenopus lae
18	2203.5	73.9	571	2 Q7ZW08	O7zw08 xenopus lae
19	2198	73.7	570	2 Q71SF8	O71sf8 gallus gall
20	2193	73.5	570	1 DPY3 MOUSE	O62188 mus musculu
21	2192	73.5	570	1 DPY3 HUMAN	O14195 homo sapien
22	2191	73.5	570	2 Q81XW6	O81xw6 homo sapien
23	2191	73.5	570	2 Q91XM8	O91xm8 rattus norv
24	2178.5	73.1	571	1 DPY3 XENLA	O13022 xenopus lae
25	2174	72.9	572	2 Q71SG3	O71sg3 gallus gall
26	2163	72.5	572	1 DPY1 MOUSE	P97427 mus musculu
27	2158	72.4	572	1 DPY1 RAT	O62950 rattus norv
28	2157	72.3	572	1 DPY1 HUMAN	O14194 homo sapien
29	2138	71.7	683	2 Q8K4H3	O8k4h3 rattus norv
30	2135	71.6	684	2 Q6DEN2	O6den2 homo sapien
31	2117	71.0	683	2 Q71SG4	O71sg4 gallus gall

RESULT 1

ID DPY4 HUMAN STANDARD; PRT; 572 AA.

AC O14531; 000240;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE Dihydropyrimidinase-related protein-4 (DRP-4)

DE mediator protein 3) (CRMP-3) (UNC33-like phosphoprotein 4) (ULIP4

DE protein).

GN Names=DPYSL4; Synonyms=CRMP3, ULIP4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Hamajima N., Kato Y., Kouwaki M., Wada Y., Sasaaki M., Nonaka M.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-553 FROM N.A.

RC TISSUE=Retina;

RX MEDLINE=98314496; PubMed=9652388;

RA Byk T., Ozon S., Sobel A.;

RT "The Ulip family phosphoproteins -- common and specific properties.";

RL Eur. J. Biochem. 254:14-24(1998).

RN [3]

RP RECOGNITION BY ANTI-CV2 AUTOANTIBODIES IN PND.

RC PubMed=10594648;

RA Honnorat J., Byk T., Kusters I., Aguerre M., Ricard D., Rogemond V.,

Quach T.T., Aunis D., Sobel A., Mattei M.-G., Kolattukudy P.E.,

Belin M.-P., Antoine J.-C.;

RT "Ulip/CRMP proteins are recognized by autoantibodies in paraneoplastic

neurological syndromes.";

RL Eur. J. Neurosci. 11:4226-4232(1999).

CC -1- FUNCTION: May be involved in the axonal growth during development

by transducing signals from different semaphorins.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -1- DISEASES: Antibodies against post-translationally modified DPYSL4,

also called anti-CV2 autoantibodies, are present in sera from

patients with paraneoplastic neurological diseases (PND). PND are

disorders of the nervous system associated with various systemic

cancers which are not a direct result of the tumor mass or

metastasis, but attributed to remote effects of the cancer.

CC -1- SIMILARITY: Belongs to the dehydropyrimidinase family.

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or send an email to license@isb-sib.ch).

O6pij1 mus musculu
Q86u75 homo sapien
Q14117 homo sapien
Q63150 rattus norv
Q642f0 rattus norv
Q9eqf5 mus musculu
Q961l1 homo sapien
Q9eqf6 mus musculu
Q9jhu0 rattus norv
Q9bpu6 homo sapien
Q62952 rattus norv
Q9jmg8 rattus norv
Q86lt3 drosophila
Q7qbkg9 anopheles g

ALIGNMENTS

32 2110 70.8 686 2 Q6PIJ1
33 1691 56.7 619 2 Q86U75
34 1556 52.2 519 1 DPYS HUMAN
35 1550 52.0 519 1 DPYS_RAT
36 1550 52.0 519 2 Q642F0
37 1520 51.0 519 1 DPYS_MOUSE
38 1492 50.0 404 2 Q961L1
39 1481.5 49.7 564 1 DPYS_MOUSE
40 1481.5 49.7 564 1 DPYS_RAT
41 1469.5 49.3 564 1 DPYS_HUMAN
42 1457 48.9 568 1 DPY3_RAT
43 1456 48.8 563 2 Q9JMG8
44 1347 45.2 594 2 Q86LT3
45 1318 44.2 595 2 Q7QBK9

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CC -----
DR EMBL; AB006713; BAA21886.1; -.
DR EMBL; Y10976; CAA71872.1; -.
DR HSSP; Q45515; 1K1D.
DR MEROPS; M38.977; -.
DR Genew; HGNC:3016; DPYSL4.
DR MTM; 608407; -.
DR GO; GO:0007399; P. neurogenesis; TAS.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
FT CONFLICT 122 122 (in Ref. 2).
SQ SEQUENCE 572 AA; 61905 MW; 3E7A33B3B5D5B8E9 CRC64;

Query Match 99.8%; Score 2978; DB 1; Length 572;
Best Local Similarity 99.8%; Pred. No. 5.1e-207;
Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFQKKSIPIRISDRLLIRGGRVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
DB 1 MSFQKKSIPIRISDRLLIRGGRVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
QY 61 HGLMVLPGGVVHTRLOMPVLGTMTPADDFCQGTAAALAGGTTMILDHVPDGTGVSLLAY 120
DB 61 HGLMVLPGGVVHTRLOMPVLGTMTPADDFCQGTAAALAGGTTMILDHVPDGTGVSLLAY 120
QY 121 EQRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDCQCSDSQ 180
DB 121 EQRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDCQCSDSQ 180
QY 181 MYIFSIIRDLGALAQVHAENGDI VEEBQKRLLELGTITGPEGHVLSHPBEVEAEVYRAV 240
DB 181 MYIFSIIRDLGALAQVHAENGDI VEEBQKRLLELGTITGPEGHVLSHPBEVEAEVYRAV 240
QY 241 TIAKQANCLYVTKVMSKGAADIAQAQRGVVVFGEPIITASLGTDGSHYWSKNWAKAA 300
DB 241 TIAKQANCLYVTKVMSKGAADIAQAQRGVVVFGEPIITASLGTDGSHYWSKNWAKAA 300
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVKGNFALIPGTNGIER 360
DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVKGNFALIPGTNGIER 360
QY 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
DB 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
QY 421 SAKTHNLNVEYNIPFEGVECHGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDVPYK 480
DB 421 SAKTHNLNVEYNIPFEGVECHGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDVPYK 480
QY 481 RIKARNRLAEIHGVPRLGYPGVHVMVPAKPGSGAPARASCPOKISVPPVRNLHSGGFS 540
DB 481 RIKARNRLAEIHGVPRLGYPGVHVMVPAKPGSGAPARASCPOKISVPPVRNLHSGGFS 540
QY 541 LSGSQADHDHIAARTAKIMAPPGSRNITSLS 572
DB 541 LSGSQADHDHIAARTAKIMAPPGSRNITSLS 572

RESULT 2
DPY4 MOUSE
ID DPY4 MOUSE STANDARD; PRT; 572 AA.
AC Q35058; Q08886;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 03-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydropyrimidinase related protein-4 (DRP-4) (Collapsin response
DE mediator protein 3) (CRMP-3) (UNC33-like phosphoprotein 4) (ULIP4
DE protein).
GN Names=Dpy414; Synonyms=Crm3, Ulip4;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Hamajima N., Kato Y., Kowaki M., Wada Y., Sasaki M., Nonaka M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=98314496; PubMed=9652388;
RA Byk T., Ozon S., Sobel A.;
RT "The Ulip family phosphoproteins -- common and specific properties.";
RL Eur. J. Biochem. 254:14-24(1998).
CC -!- FUNCTION: May be involved in the axonal growth during development
CC by transducing signals from different semaphorins.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the dehydroxyrimidinase family.
CC -----
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CC -----
DR EMBL; AB006715; BAA21888.1; -.
DR EMBL; Y09079; CAA70299.1; -.
DR HSSP; Q45515; 1K1D.
DR MEROPS; M38.977; -.
DR MGD; MGI:1349764; Dpysl4.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
FT CONFLICT 125 126 ER -> DG (in Ref. 2).
FT CONFLICT 354 354 G -> V (in Ref. 2).
FT CONFLICT 420 420 F -> I (in Ref. 2).
SQ SEQUENCE 572 AA; 61961 MW; 37671129FC02C7AF CRC64;

Query Match 94.7%; Score 2824; DB 1; Length 572;
Best Local Similarity 93.2%; Pred. No. 7.3e-196;
Matches 533; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSFQKKSIPIRISDRLLIRGGRVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
DB 1 MSFQKKSIPIRISDRLLIRGGRVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
QY 61 HGLMVLPGGVVHTRLOMPVLGTMTPADDFCQGTAAALAGGTTMILDHVPDGTGVSLLAY 120
DB 61 HGLMVLPGGVVHTRLOMPVLGTMTPADDFCQGTAAALAGGTTMILDHVPDGTGVSLLAY 120
QY 121 EQRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDCQCSDSQ 180
DB 121 EQRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDCQCSDSQ 180
QY 181 MYIFSIIRDLGALAQVHAENGDI VEEBQKRLLELGTITGPEGHVLSHPBEVEAEVYRAV 240
DB 181 MYIFSIIRDLGALAQVHAENGDI VEEBQKRLLELGTITGPEGHVLSHPBEVEAEVYRAV 240
QY 241 TIAKQANCLYVTKVMSKGAADIAQAQRGVVVFGEPIITASLGTDGSHYWSKNWAKAA 300
DB 241 TIAKQANCLYVTKVMSKGAADIAQAQRGVVVFGEPIITASLGTDGSHYWSKNWAKAA 300
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVKGNFALIPGTNGIER 360
DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVKGNFALIPGTNGIER 360
QY 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
DB 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420

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Db 361 RMSVWEKCVASGMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPRATKVF 420
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Db 421 SAKSHNLNVEYNIPEGVECRGAPAVVISQGRVLEEDGKMFVTPGAGRFVPRKTPFPDPVYK 480
QY 481 RIKARNRLAEIHGVPRLGDPVHEVWVPAPKPGSGAPARASCPOKISVPPVRNLHQSGGFS 540
Db 481 RIKARNRLAEIHGVPRLGDPVHEVWVPAPKPGSGAPARASCPOKISVPPVRNLHQSGGFS 540
QY 541 LSGSQADHDHARRTAQKIMAPPGGRSNTLS 572
Db 541 LSGSQADHDHARRTAQKIMAPPGGRSNTLS 572

RESULT 3
DPY4 RAT
ID DPY4 RAT
AC Q62951;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydropyrimidinase related protein-4 (DRP-4) (Collapsin response
DE mediator protein 3) (CRMP-3) (UNC33-like phosphoprotein 4) (ULIP4
DE protein) (Fragment).
OS Names=Dpye14; Synonyms=Crmp3, Ulip4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96424532; PubMed=8815901;
RA Wang L.; Strittmatter S.M.;
RT "A family of rat CRMP genes is differentially expressed in the nervous
RT system."
RL J. Neurosci. 16:6197-6207(1996).
CC -1- FUNCTION: May be involved in the axonal growth during development
CC by transducing signals from different semaphorins.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- DEVELOPMENTAL STAGE: Expressed transiently in developing spinal
CC cord and selectively in the postnatal cerebellum.
CC -1- SIMILARITY: Belongs to the dehydropyrimidinase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U52103; AB03281.1; -
DR HSP; Q45515; IK1D.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
FT NON TER
SQ SEQUENCE 564 AA; 61085 MW; 42050891CC1436D2 CRC64;
Query Match 93.7%; Score 2795; DB 1; Length 564;
Best Local Similarity 93.4%; Pred. No. 9e-194;
Matches 527; Conservative 21; Mismatches 16; Indels 0; Gaps 0;
QY 9 IPRITSDRLIRGRIWVNDQSFVADVHVEDGLIKQIGENLIVPGGKTTIDAGLWVLP 68
Db 1 IPRITSDRLIRGRIWVNDQSFVADVHVEDGLIKQIGENLIVPGGKTTIDAGLWVLP 60
QY 69 GVDVHTRLOMPVLGMPADDFCQGTAAALAGGTTMLDHFVPPDTGVSLLAAYEQWRRERAD 128

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Db 61 GVDVHTRLOMPVLGMPADDFCQGTAAALAGGTTMLDHFVPPDTGVSLLAAYEQWRRERAD 120
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Db 121 SAACDYSLHVDITRWHESIKELEALVREKGVNSFLVFMAYKDRQCQSDSQMYEIFSII 180
QY 189 RDLGALAQAHAENGDIIVEBEQKRLLEIGITGPGEHVLSPHEVEABAVRAVTIAKOANC 248
Db 181 RDLGAVAQAHAENGDIIVEBEQKRLLEIGITGPGEHVLSPHEVEABAVRAVTIAKOANC 240
QY 249 PLYVTKVMSKGADATAQAKRGVGVVFGPITASLTGDSHYWSKWAKAAAVTSPPVN 308
Db 241 PLYITTKVMSKGADAMVAQARRGVVFGPITASLTGDSHYWSKWAKAAAVTSPPIN 300
QY 309 PDPTTADHLTCLISSGDLQVTSAGHCTFTTAQKAVGKDFALIPGEGTNGIEERMSVWWEK 368
Db 301 PDPTTADHLTCLISSGDLQVTSAGHCTFTTAQKAVGKDFALIPGEGTNGIEERMSVWWEK 360
QY 369 CVASGMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPRATKVIISAKTHNLN 428
Db 361 CVASGMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPRATKVIISAKSHNLN 420
QY 429 VEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTPFPDPVYKIKARNRL 488
Db 421 VEYNIPEGVECRGAPAVVISQGRVLEEDGKMFVTPGAGRFVPRKTPFPDPVYKIKARNRL 480
QY 489 AEIHGVPRLGDPVHEVWVPAPKPGSGAPARASCPOKISVPPVRNLHQSGFSLSGQADD 548
Db 481 AEIHGVPRLGDPVHEVWVPAPKPGSGAPARASCPOKISVPPVRNLHQSGFSLSGQADD 540
QY 549 HIARRTAQKIMAPPGGRSNTLS 572
Db 541 HIARRTAQKIMAPPGGRSNTLS 564

RESULT 4
Q9DDZ6
ID Q9DDZ6 PRELIMINARY; PRT; 574 AA.
AC Q9DDZ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collapsin response mediator protein-3B.
DE Names=CRMP3B;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=20545548; PubMed=10956643; DOI=10.1074/jbc.M003277200;
RA Fukada M., Watake I., Yuasa-Kawada J., Kawachi H., Kuroiwa A.,
RA Matsuda Y., Noda M.;
RT "Molecular characterization of CRMP5, a novel member of the collapsin
RT response mediator protein family."
RL J. Biol. Chem. 275:37957-37965(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22699123; PubMed=12814366;
RA Yuasa-Kawada J., Suzuki R., Kano F., Ohkawara T., Murata M., Noda M.;
RT "Axonal morphogenesis controlled by antagonistic roles of two CRMP
RT subtypes in microtubule organization."
RL Eur. J. Neurosci. 17:2329-2343(2003).
DR EMBL; AF249294; AAG37997.1; -
DR HSP; P97427; 1KCX.
DR GO; GO:0016787; F; Hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.

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DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 574 AA; 62070 MM; 96B17AC0E96CASF4 CRC64;

Query Match      84.5%; Score 2519; DB 2; Length 574;
Best Local Similarity 81.4%; Pred. No. 9.1e-174;
Matches 467; Conservative 57; Mismatches 48; Indels 2; Gaps 1;

QY 1 MSFGKKSIPRITSRLLIRGGRIVNDQSFYADVHVDEGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSNPGKSGRGTSEQLLKGKIVNDQSFYADIVVEDGLIKQIGENLAVPSGVRITDA 60

QY 61 HGLMVLPGGVVHTRIQMPVLGTPADDFCQGTKAALAGGTTMILDHVPDPTGVSLLAAY 120
DB 61 YGQLVVPGGIDVHTRIQMAVMGASADDFVQGTTRAALAGGTTMIDHVLPEAGTSLAAY 120

QY 121 EQWRERADSAACDYSLSHVDITWHSIEKELEALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
DB 121 EQWRERADSRACCDYALHIDIPRWHSIEKELEALVKEKGVNSFLVPMAYKDRCCQSDSQ 180

QY 181 MYEIPSTIIRDLGALAOVHAENGDIIVSEBOKRLLELGTGPEGHVLSHPREVRAEAVYRAV 240
DB 181 MYEIFCIIRDLGALAOVHAENGDIIEBOKRLLELGTGPEGHVLSHPREVRAEAVYRAI 240

QY 241 TIAQANCPLYVTKVMSKGAADAIQAQKRGVVVFGEPIITASLGTDGSHYWSKNWAKAAA 300
DB 241 TIAQANCPLYVTKVMSKGAADAIQAQKRGVVVFGEPIITASLGTDGSHYWSKNWAKAAA 300

QY 301 FVTSPPVNDPTTADHLTCLSSGDLQVTSAGHCTTTAAQAVKGNFALIPGTNGIEE 360
DB 301 FVTSPPVNDPTTADHLTCLSSGDLQVTSAGHCTTTAAQAVKGNFALIPGTNGIEE 360

QY 361 RMSWMEKCVASGKMDENFVATSTNAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
DB 361 RMAIWEKCVASGKMDENFVATSTNAKIFNFPYPRKGRVAVGSDADLVINWPKATKVI 420

QY 421 SAKTHNLNVEYNIIFEGVECRGAPAVVISQGRVLEDKGMFVTPGAGRFVPRKTFPDPVYK 480
DB 421 SAKTHNLNVEYNIIFEGVECRGAPAVVISQGRVLEDKGMFVTPGAGRFVPRKTFPDPVYK 480

QY 481 RIKARNLRLAIIHVGPRGLYDGPVHVWPAK--PGSGAPARASCPOKISVPPVRNLHQSG 538
DB 481 RIKARNLRLAIIHVGPRGLYDGPVHVWPAK--PGSGAPARASCPOKISVPPVRNLHQSG 540

QY 539 FSLSGSQADDDHARRTAQKIMAPPGSRNITSLS 572
DB 541 FSLSGSQADDDHARRTAQKIMAPPGSRNITSLS 574

RESULT 5
Q718G0 PRELIMINARY; PRT; 650 AA.
AC Q718G0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Collapsin response mediator protein-3A.
GN Name=CRMP3A;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2699123; PubMed=12814366;
RA Yuasa-Kawada J., Suzuki R., Kano F., Ohkawara T., Murata M., Noda M.;
RT "Axonal morphogenesis is controlled by antagonistic roles of two CRMP
RL subtypes in microtubule organization."
RL Eur. J. Neurosci. 17:2329-2343(2003).
DR EMBL; AF301551; AAQ14489.1; -
DR HSSP; P97427; 1KCX.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.

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DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 650 AA; 69561 MM; E1FAB72370C26A4D CRC64;

Query Match      83.4%; Score 2488; DB 2; Length 650;
Best Local Similarity 81.8%; Pred. No. 1.9e-171;
Matches 459; Conservative 56; Mismatches 44; Indels 2; Gaps 1;

QY 14 SRLLIRGRIVNDQSFYADVHVDEGLIKQIGENLIVPGGIKTIDAHGLMVLPGGVVH 73
DB 90 SEQLLKGKIVNDQSFYADIVVEDGLIKQIGENLAVPSGVRITDAVYQQLVVPGGIDVH 149

QY 74 TRLQMPVLGTPADDFCQGTKAALAGGTTMILDHVPDPTGVSLLAAYEOWRERADSAAC 133
DB 150 TRLQMAVMGASADDFVQGTTRAALAGGTTMIDHVLPEAGTSLAAYEOWRERADSAAC 209

QY 134 DYSLSHVDITWHSIEKELEALVKEKGVNSFLVPMAYKDRCCQSDSQSYEISIRDLGA 193
DB 210 DYALHIDIPRWHSIEKELEALVKEKGVNSFLVPMAYKDRCCQSDSQSYEISIRDLGA 269

QY 194 LAQVHAENGDIIVSEBOKRLLELGTGPEGHVLSHPREVRAEAVYRAVTTIAQANCPLYV 253
DB 270 LAQVHAENGDIIEBOKRLLELGTGPEGHVLSHPREVRAEAVYRAITTTIAQANCPLYV 329

QY 254 KVMKGAADAIQAQKRGVVVFGEPIITASLGTDGSHYWSKNWAKAAAFTSPVNDPTT 313
DB 330 KIMSKAADVVAQAQKRGVVVFGEPIITASLGTDGSHYWSKNWAKAAAFTSPVNDPTT 389

QY 314 ADHLTCLSSGDLQVTSAGHCTTTAAQAVKGNFALIPGTNGIEE RMSWMEKCVASG 373
DB 390 PERLSGLSSGDLQVAGSAHCTTTAAQAVKGNFALIPGTNGIEE RMSWMEKCVASG 449

QY 374 KMDENFVATSTNAKIFNFPYPRKGRVAVGSDADLVINWPKATKIIISAKTHNLNVEYNI 433
DB 450 KMDENFVATSTNAKIFNFPYPRKGRVAVGSDADLVINWPKATKIIISAKTHNLNVEYNI 509

QY 434 FEGVECRGAPAVVISQGRVLEDKGMFVTPGAGRFVPRKTFPDPVYKRIKARNLRLAIIH 493
DB 510 FEGTECHGAPAVVISQGRVLEDKGMFVTPGAGRFVPRKTFPDPVYKRIKARNLRLAIIH 569

QY 494 VPRGLYDGPVHVWPAK--PGSGAPARASCPOKISVPPVRNLHQSGFSLSGSQADDDH 551
DB 570 VPRGLYDGPVHVWPAK--PGSGAPARASCPOKISVPPVRNLHQSGFSLSGSQADDDH 629

QY 552 RRTAQKIMAPPGSRNITSLS 572
DB 630 RRTAQKIMAPPGSRNITSLS 650

RESULT 6
Q72TP7 PRELIMINARY; PRT; 668 AA.
AC Q72TP7
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE MGC53768 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klauschen R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellon N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Jones S.J., Marra M.A., RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2] RN SEQUENCE FROM N.A. RP TISSUE=Embryo; RC TISSUE=Embryo; RX MDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., RA ENBL; BC043880; AA043880.1; -. DR HSP; P97427; IKCX. DR GO:0016787; F:hydrolase activity; IEA. DR InterPro; IPR006680; Amidohydro_1. DR InterPro; IPR005847; DHOase. DR InterPro; IPR011059; Metallo_hydrolase. DR Pfam; PF01979; Amidohydro_1; 1. DR ProDom; PD000518; DHOase; 1. SQ SEQUENCE 668 AA; 72485 MW; AB3994D680E3B500 CRC64;

Query Match 81.9%; Score 2441.5; DB 2; Length 668; Best Local Similarity 79.5%; Pred. No. 4.7e-168; Indels 1; Gaps 1; Matches 445; Conservative 67; Mismatches 47

QY 14 SDRLIRGRINVDQSFYADHVHEDGLIKQIGENLVPGGIKTIDAGHLMVLPFGVDVH 73
DB 109 SDRLIRGGKI VDDQSFADIVIEDGLIKQIGENLVPGGVKTIDAGHLMVLPFGVDVH 168

QY 74 TRLOMPVLGTPADDPCQGTAAALAGGTTMILDHVPDPTGVSLAAAYEQWRERADSAAC 133
DB 169 TRLOMPVVGMTSADDPFQGTAAALAGGTTMIDHVPFNSGNLVQAYDQWRWADGSVCC 228

QY 134 DYSLVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSOMYEIPISTIRDLGA 193
DB 229 DYSLVHVDITRWHSLSKEELEALVKDGVNSFLVPMAYKEQYQCTDAEMEIFSIIRLGA 288

QY 194 LAQVHAENGDI VBEQKRLLELGTGPEGHVLSHPERVAEAVVAVTIAKQANCPLYVT 253
DB 289 IAQVHAENGDI IQEQRKMLECGITGPEGHVLSHPERVAEAAFRATIAKQANCPLYIT 348

QY 254 KVMKGAADAIAQKRGGVVVGFEPITASIGTGSHYWSKNWAKAAAFVTSPPVNPDPPT 313
DB 349 KVMRGAADVIAQKRGGIVVYGETLPASIGTGTWYWSKNWAKAAAFVTSPPISDPST 408

QY 314 ADHLTCLSSGDLQVTSASCTPTTAQKAVGNKFNALIPEGTNGIERMSWWEKCVASG 373
DB 409 PDLTCLSSGDLQVTSASCTPTTAQKAVGNKFNALIPEGTNGIERMTIWDKCVTSG 468

QY 374 KMDENEFVAVTSNAAKIFNYPKRGVAVGSDADLVINWPKATKIISAKTHLNVEYNI 433
DB 469 KMDENAFVAVTSNAAKLFNYPKRGRIAGSDADLVINWPKTKAKIISAKTHNVAELNI 528

QY 434 FEGVECRGAPAVVISQGRVALEDKMFPVTPGAGRFVPRKTPPDVYVKRIKARNLAEIHG 493
DB 434 FEGVECRGAPAVVISQGRVLEKMGVNSFLVPMAYKRCQCSDSQ 180

QY 121 EOWREADSAACDYSLVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSQ 180
DB 121 DQWRWADSKSCDYSLVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSQ 180

QY 181 MVEIFSIIRDLGALAQVHAENGDI VBEQKRLLELGTGPEGHVLSHPERVAEAVVAV 240

Db 529 FEGMECYGAPEVVVISQGRVLEKMGVNSFLVPMAYKRCQCSDSQ 180

QY 494 VPRGLYDGPVHVMYPAKPGSGAPA-RASCPGKISVPPVNLHOSGFSLSGSQADHIAH 552
DB 589 VPRGLYDGPVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSQ 180

QY 553 RTAQKIMAPPGGRSNTISLS 572
DB 649 RTTQKIVAPPGGRSNTISLS 668

RESULT 7
DPY2_CHICK
ID DPY2_CHICK STANDARD; PRT; 572 AA.
AC Q90635;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Dihydropyrimidinase related protein-2 (DRP-2) (Collapsin response mediator protein CRMP-62).
OS Gallus gallus (Chicken).
OC Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglion;
RX MEDLINE=95364923; PubMed=7637782; DOI=10.1038/376509a0; Goshima Y., Nakamura F., Strittmatter P., Strittmatter S.M.; RT "Collapsin-induced growth cone collapse mediated by an intracellular protein related to UNC-33."; RT Nature 376:509-514(1995).
CC -!- FUNCTION: Involved in neuronal growth cone collapse.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the dehydropyrimidinase family.
CC -----
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CC -----
CC EMBL; U17277; AAA93200.1; -.
DR PIR; S58889; S58889.
DR HSP; Q45515; IKID.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 572 AA; 62330 MW; 85DB9E3DD5E54D8D CRC64;

Query Match 79.4%; Score 2368; DB 1; Length 572; Best Local Similarity 76.5%; Pred. No. 7.9e-163; Indels 0; Gaps 0; Matches 437; Conservative 68; Mismatches 66

QY 1 MSFGQKKSIPRITSRLIRGRINVDQSFYADHVHEDGLIKQIGENLVPGGIKTIDA 60
DB 1 MSVQKKNIPIRITSRLIRGGKI VDDQSFADIVIEDGLIKQIGENLVPGGVKTIEA 60

QY 61 HGLMVLPGVDVHTRLOMPVLGTPADDPCQGTAAALAGGTTMILDHVPDPTGVSLAA 120
DB 61 HGRMVIPGGIDVHTRFQMPQEGMTSADDPFQGTAAALAGGTTMIDHVPPEPGTSLTAF 120

QY 121 EOWREADSAACDYSLVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSQ 180
DB 121 DQWRWADSKSCDYSLVHVDITRWHSIKEELEALVKEGVNSFLVPMAYKRCQCSDSQ 180

QY 181 MVEIFSIIRDLGALAQVHAENGDI VBEQKRLLELGTGPEGHVLSHPERVAEAVVAV 240

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Db      181 IYEVLSVIRDIGATAQVHAENGDIABEQORILELGIITGPEGHVLSRPEVEAEAVNRAI 240
QY      241 TIAQANCPLYTVKWSKGAADIAIAQAKRGVVVFGPEPTASLGTGSHYWSKNWAKAAA 300
Db      241 TIANQNCPLIYTVKWSKSAAEVIAQARKKGTGVYGEPTASLGTGSHYWSKNWAKAAA 300
QY      301 FVTSPPVNDPTTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPEGTNGIEE 360
Db      301 FVTSPPVNDPTTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPEGTNGIEE 360
QY      361 RMSWVEKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
Db      361 RMSIWDKAVVTKMDENQFVAVTSTNAAKIFNLYPRKGRIAVGSDADLVINDPDSVKTI 420
QY      421 SAKTHNLAVENYIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTPFPDVYK 480
Db      421 SAKTHNISLEYNIFEGMECRGSPLVVISQKIVLEDGNLHVTEGSGRYTPRKFPDPVYK 480
QY      481 RIKARNRLAEIHGVPRLGVDGVPVHVMPAKPGSGAPARASCPCGKISVPPVRLNHOSGFS 540
Db      481 RIKARSLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQQAAPPVRLNHOSGFS 540
QY      541 LSGSQADDDHARRTAQKIMAPPGGRSNITSL 571
Db      541 LSGAQIDDDNIPTTQRIIVAPPGGRANITSL 571

RESULT 8
Q719G1 PRELIMINARY; PRT; 572 AA.
AC Q719G1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Collapsin response mediator protein-2B.
GN Names=CRMP2B;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22699123; PubMed=12814366;
RA Yuasa-Kawada J., Suzuki R., Kano F., Okawara T., Murata M., Noda M.;
RT "Axonal morphogenesis controlled by antagonistic roles of two CRMP
subtypes in microtubule organization.";
RL Eur. J. Neurosci. 17:2329-2343(2003).
DR EMBL; AF301550; AAQ14488.1; -.
DR HSSP; P97427; IKCX.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_like.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 572 AA; 62258 MW; 07DB9D888306F8DB CRC64;

Query Match 79.2%; Score 2361; DB 2; Length 572;
Best Local Similarity 76.4%; Pred. No. 2.5e-162;
Matches 436; Conservative 68; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGKKSIPIRTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
Db 1 MSVQGGKNIPRTISDRLLIKGGKIVNDQSFYADIYMEDGLIKQIGENLIVPGGVKTIEA 60
QY 61 HGLMVLPGGVVDVHTRIQMPVLGTMTPADDPCQGTAAALAGTTTILDRHVPDGTGSLAA 120
Db 61 HGRMVLPGGIDVHTRIQMPVQGGMTSADDPFGQTKAALAGTTTIIIDHVVPEPGTSLTAF 120

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QY      121 EOWBRADSAACDYSLHVDITRMHESIKEELEALVKKEGVNSFLVFMAYKDRCCQSDSQ 180
Db      121 DQWRWALWSKSCDYSLHVDITRMHKGVEEALVKDHGVNSFLVYMAKDRPQLSDSQ 180
QY      181 MYEIPSIIRDLGALAQVHAENGDIABEQORILELGIITGPEGHVLSRPEVEAEAVNRAI 240
Db      181 IYEVLSVIRDIGATAQVHAENGDIABEQORILELGIITGPEGHVLSRPEVEAEAVNRAI 240
QY      241 TIAQANCPLYTVKWSKGAADIAIAQAKRGVVVFGPEPTASLGTGSHYWSKNWAKAAA 300
Db      241 TIANQNCPLIYTVKWSKSAAEVIAQARKKGTGVYGEPTASLGTGSHYWSKNWAKAAA 300
QY      301 FVTSPPVNDPTTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPEGTNGIEE 360
Db      301 FVTSPPVNDPTTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPEGTNGIEE 360
QY      361 RMSWVEKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
Db      361 RMSIWDKAVVTKMDENQFVAVTSTNAAKIFNLYPRKGRIAVGSDADLVINDPDSVKTI 420
QY      421 SAKTHNLAVENYIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTPFPDVYK 480
Db      421 SAKTHNISLEYNIFEGMECRGSPLVVISQKIVLEDGNLHVTEGSGRYTPRKFPDPVYK 480
QY      481 RIKARNRLAEIHGVPRLGVDGVPVHVMPAKPGSGAPARASCPCGKISVPPVRLNHOSGFS 540
Db      481 RIKARSLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQQAAPPVRLNHOSGFS 540
QY      541 LSGSQADDDHARRTAQKIMAPPGGRSNITSL 571
Db      541 LSGAQIDDDNIPTTQRIIVAPPGGRANITSL 571

RESULT 9
DPY2_BOVIN STANDARD; PRT; 572 AA.
AC O02675;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydropyrimidinase related protein-2 (DRP-2) (Neural specific protein
DE NSP60).
GN Name=DPSL2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Ruminantia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamata T.K.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the dehydropyrimidinase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U83278; AAB80618.1; -.
DR HSSP; Q45515; 1KID.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 572 AA; 62277 MW; 343507ACB9D91BDE CRC64;

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Query Match		78.9%; Score 2353; DB 1; Length 572;
Best Local Similarity		75.8%; Pred. No. 9.6e-162;
Matches 433; Conservative 72; Mismatches 66; Indels 0; Gaps 0;		
Qy	1	MSFGKKSIPIRTSDRLIRGRVNDQSFYADVHVEDGLIKQIGENLVPGGIKTIDA 60
Db	1	MSVQKKNIPIRTSDRLIRGGKIVNDQSFYADIYMEDGLIKQIGENLVPGGVKTIEA 60
Qy	61	HGLMVLPGVDVHTRLOMPVLGMPADDFQCGTKAALAGGTTMLDHRVDPDTGVSLLAA 120
Db	61	HSRMVPGGIDVHTRFQMPDQGMTSADDFQGTAKAALAGGTTMLDHRVDPDTGVSLLAA 120
Qy	121	EQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRCCSDSQ 180
Db	121	DQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRFQLTDSQ 180
Qy	181	MYEIFSIRDLGALAOVHAENGDIYVEEQKRLLELIGITGPEGHVLSHPREVEAEVAV 240
Db	181	IYEVLSVIRDIGALAOVHAENGDIYAEQQRIIDLGITGPEGHVLSHPREVEAEVAVRSI 240
Qy	241	TIKQANCPLYVTKWSKGAADIAQAQRKRGVVVFGPEPITASLGTDGSHYWSKNWAKAAA 300
Db	241	TIANTQNCPLYVTKWSKSAAEVIAQAQRKGTVVYGEPIITASLGTDGSHYWSKNWAKAAA 300
Qy	301	FVTSPPVNPDPPTADHILTCLLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTNGIEE 360
Db	301	FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKONFTLIPGTNGTEE 360
Qy	361	RMSVMWEKCVASGKMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPNKATKII 420
Db	361	RMSVWIDKAVVTGMDNEFVAVTSTNAAKFVNLVYPRKGRISVGSADLVINPDSVKTI 420
Qy	481	RIKARNRLABIHGVRGLYDGPVHVWVPAKPGSGAPARASCPCGKISVPPVRLHSGGFS 540
Db	481	RIKARSLAELRGVPRGLYDGPVCEVSVTPKVTTPASSAKTSPAKQOAPVPRNLHSGGFS 540
Qy	541	LSGSQADDDHARTTAQKIMAPPGGRANITSL 571
Db	541	LSGAQIDDDNIPTTQRIQVAPPQGRANITSL 571
RESULT 10		
ID	DPY2_RAT	
AC	P47942;	STANDARD; PRT; 572 AA.
DT	01-FEB-1996 (Rel. 33, Created)	
DT	01-FEB-1996 (Rel. 33, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Dihydropyrimidinase related protein-2 (DRP-2) (Turned on after division; 64 kDa protein) (TOAD-64) (Collapsin response mediator protein 2) (CRMP-2).	
DE	protein 2) (CRMP-2).	
GN	Names=Dpy812;	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=101116;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 136-142; 402-418; 441-450 AND 499-511.	
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;	
RX	MEDLINE=96033765; PubMed=7472434;	
RA	Minturn J.B., Fryer H.J.L., Geschwind D.H., Hockfield S.;	
RT	"TOAD-64", a gene expressed early in neuronal differentiation in the rat, is related to unc-33, a C. elegans gene involved in axon outgrowth.";	
RT	J. Neurosci. 15:6757-6766(1995).	
RL	J. Neurosci.	
CC	-I- FUNCTION: May have a role in axon elaboration.	
CC	-I- SUBCELLULAR LOCATION: Tightlly, but noncovalently, associated with membranes.	
Query Match		78.8%; Score 2349; DB 1; Length 572;
Best Local Similarity		76.0%; Pred. No. 1.9e-161;
Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;		
Qy	1	MSFGKKSIPIRTSDRLIRGRVNDQSFYADVHVEDGLIKQIGENLVPGGIKTIDA 60
Db	1	MSVQKKNIPIRTSDRLIRGGKIVNDQSFYADIYMEDGLIKQIGENLVPGGVKTIEA 60
Qy	61	HGLMVLPGVDVHTRLOMPVLGMPADDFQCGTKAALAGGTTMLDHRVDPDTGVSLLAA 120
Db	61	HSRMVPGGIDVHTRFQMPDQGMTSADDFQGTAKAALAGGTTMLDHRVDPDTGVSLLAA 120
Qy	121	EQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRCCSDSQ 180
Db	121	DQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRFQLTDSQ 180
Qy	181	MYEIFSIRDLGALAOVHAENGDIYVEEQKRLLELIGITGPEGHVLSHPREVEAEVAV 240
Db	181	IYEVLSVIRDIGALAOVHAENGDIYAEQQRIIDLGITGPEGHVLSHPREVEAEVAVRSI 240
Qy	241	TIKQANCPLYVTKWSKGAADIAQAQRKRGVVVFGPEPITASLGTDGSHYWSKNWAKAAA 300
Db	241	TIANTQNCPLYVTKWSKSAAEVIAQAQRKGTVVYGEPIITASLGTDGSHYWSKNWAKAAA 300
Qy	301	FVTSPPVNPDPPTADHILTCLLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTNGIEE 360
Db	301	FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKONFTLIPGTNGTEE 360
Qy	361	RMSVMWEKCVASGKMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPNKATKII 420
Db	361	RMSVWIDKAVVTGMDNEFVAVTSTNAAKFVNLVYPRKGRISVGSADLVINPDSVKTI 420
Qy	421	SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPPFVYK 480
Db	421	SAKTHNSLEYNIPEGMECRGSLVVISQGVILEDTLHVTEGSGRYIPRKFPPFVYK 480
Qy	481	RIKARNRLABIHGVRGLYDGPVHVWVPAKPGSGAPARASCPCGKISVPPVRLHSGGFS 540
Db	481	RIKARSLAELRGVPRGLYDGPVCEVSVTPKVTTPASSAKTSPAKQOAPVPRNLHSGGFS 540
Qy	541	LSGSQADDDHARTTAQKIMAPPGGRANITSL 571
Db	541	LSGAQIDDDNIPTTQRIQVAPPQGRANITSL 571
RESULT 11		
ID	Q6P5D0	PRELIMINARY; PRT; 572 AA.

CC -I- DEVELOPMENTAL STAGE: Expressed immediately after neuronal birth and is dramatically down-regulated in the adult.
CC -I- SIMILARITY: Belongs to the dehydroxymethylase family.
CC
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CC EMBL; Z46882; CAA86981.1; -
DR PIR; A59280; S49985.
DR HSSP; Q45515; 1K1D.
DR RGD; 2517; Dpy812.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.
DR ProDom; PD000518; DHOase; 1.
KW Direct protein sequencing.
SQ SEQUENCE 572 AA; 62277 MW; C031P3BC039AA737 CRC64;

Query Match 78.8%; Score 2349; DB 1; Length 572;
Best Local Similarity 76.0%; Pred. No. 1.9e-161;
Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

Qy 1 MSFGKKSIPIRTSDRLIRGRVNDQSFYADVHVEDGLIKQIGENLVPGGIKTIDA 60
Db 1 MSVQKKNIPIRTSDRLIRGGKIVNDQSFYADIYMEDGLIKQIGENLVPGGVKTIEA 60
Qy 61 HGLMVLPGVDVHTRLOMPVLGMPADDFQCGTKAALAGGTTMLDHRVDPDTGVSLLAA 120
Db 61 HSRMVPGGIDVHTRFQMPDQGMTSADDFQGTAKAALAGGTTMLDHRVDPDTGVSLLAA 120
Qy 121 EQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRCCSDSQ 180
Db 121 DQWRERADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVPMAYKDRFQLTDSQ 180
Qy 181 MYEIFSIRDLGALAOVHAENGDIYVEEQKRLLELIGITGPEGHVLSHPREVEAEVAV 240
Db 181 IYEVLSVIRDIGALAOVHAENGDIYAEQQRIIDLGITGPEGHVLSHPREVEAEVAVRSI 240
Qy 241 TIKQANCPLYVTKWSKGAADIAQAQRKRGVVVFGPEPITASLGTDGSHYWSKNWAKAAA 300
Db 241 TIANTQNCPLYVTKWSKSAAEVIAQAQRKGTVVYGEPIITASLGTDGSHYWSKNWAKAAA 300
Qy 301 FVTSPPVNPDPPTADHILTCLLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTNGIEE 360
Db 301 FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKONFTLIPGTNGTEE 360
Qy 361 RMSVMWEKCVASGKMDNEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINPNKATKII 420
Db 361 RMSVWIDKAVVTGMDNEFVAVTSTNAAKFVNLVYPRKGRISVGSADLVINPDSVKTI 420
Qy 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPPFVYK 480
Db 421 SAKTHNSLEYNIPEGMECRGSLVVISQGVILEDTLHVTEGSGRYIPRKFPPFVYK 480
Qy 481 RIKARNRLABIHGVRGLYDGPVHVWVPAKPGSGAPARASCPCGKISVPPVRLHSGGFS 540
Db 481 RIKARSLAELRGVPRGLYDGPVCEVSVTPKVTTPASSAKTSPAKQOAPVPRNLHSGGFS 540
Qy 541 LSGSQADDDHARTTAQKIMAPPGGRANITSL 571
Db 541 LSGAQIDDDNIPTTQRIQVAPPQGRANITSL 571

RESULT 11
Q6P5D0
ID Q6P5D0 PRELIMINARY; PRT; 572 AA.

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AC Q6P5D0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dihydropyrimidinase-like 2.
GN Names=Dpyvsl2;
OS Mus musculus (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062955; AAH62955.1; -.
DR HSP; P97427; 1KX.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_like.
DR InterPro; IPR005847; DHOase.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD000518; DHOase; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 572 AA; 62277 MW; C031F3BC038AA737 CRC64;

Query Match 78.8%; Score 2349; DB 2; Length 572;
Best Local Similarity 76.0%; Pred. No. 1.9e-161;
Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

Qy 1 MSFGKKSIPRTSDRLITGGRIIVNDQSPYADVHVEGLIKOIGENLVPGIKTIDA 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MSYGGKKNIPRTSDRLITGGRIIVNDQSPYADIVMEDGLIKOIGENLVPGVKTEIA 60

Qy 61 HGLMVLPGGVVHTRQLQMPVLGTPADDFCQGTAKALAGGTTMIDHVPDGTGSLAAV 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 HSRMVLPGGIDVHTRQMPDQMTSADDPFGTKAALAGGTTMIDHVPDGTGSLAAV 120

Qy 121 EQWRERADSAACDYSLSHVDITWHSIKIEELALVKKGKGVNLFVPMAYKDRCCSDSQ 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 DQWRERADSKSCDYSLSHVDITWHSIQEELALVKKGKGVNLFVPMAYKDRFQLTDSQ 180

Qy 181 MYEIPSLIDGLAQVHAENGDIVEEOKGLELGTGEGHVLSPHEVEAEVYRAV 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 IYELVSLVIRDIGIAQVHAENGDIIEEQRIIDLGTGEGHVLSPHEVEAEVYRNSI 240

Qy 241 TIAQANCPLYVTYKMSKGAADIAQAQRGVVVFGEPIPTASLGTQDSHYWSKNWAKAAA 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DR Pfam; PF01979; Amidohydro 1; 1.
DR ProDom; PD001248; Amidohydro 1; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 572 AA; 62170 MW; 7FDAE8A242ACF62D CRC64;

Query Match      78.2%; Score 2331; DB 1; Length 572;
Best Local Similarity 75.5%; Pred. No. 3.8e-160;
Matches 431; Conservative 70; Mismatches 70; Indels 0; Gaps 0;

QY 1 MSFGKKSIPIRITSDRLIRGRVNDQSFYADVHVDEGLIKQIGENLIVPGGIKTIDA 60
Db 1 MSYQKKNIPITSDRLIRGRVNDQSFYADVHVDEGLIKQIGENLIVPGGIKTIEA 60
QY 61 HGLMVLPGGVVHTRLOMPVLGMPADDFCGTGAALAGGTTMLDHDVFPDPTGVSLAA 120
Db 61 HSRMVLPGGIDVHTRFQMPQOGMTSADDFGTTGAALAGGTTMIIDHVVPDPTGVSLAA 120
QY 121 EQWREADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCSDSQ 180
Db 121 DQWREADSKSCDYSLSHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCSDSQ 180
QY 181 MYEIFSIRDLGALAQAHAENGDI VEEBQKRLLELGTGPEGHVLSPHEVEAEAVYRA 240
Db 181 IYEVLSVIRDIGAIAQAHAENGDI IAEAQORILDGLGTGPEGHVLSPHEVEAEAVNRSI 240
QY 241 TIAKQANCLVYTKVMSKGAADAIQAQRGVVVFGEPI TASIGTDSHYMSKNAKAA 300
Db 241 TIANQNCPLVYTKVMPKSAEAVIAQARKKGTVYGEPI TASIGTDSHYMSKNAKAA 300
QY 301 FVTSPPVNPDPPTADHLTCLLSGGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIE 360
Db 301 FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIE 360
QY 361 RMSWWEKCVASGKNDENEFVATSTNAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
Db 361 RMSVIMDKAVVTGKMDENQFVATSTNAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
QY 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYK 480
Db 421 SAKTHNSALEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYK 480
QY 481 RIKARNLRLAEIHGVPRLGYPVHEVMVPAKPGSGAPARASCPGKISVPPVRLNHQSGFS 540
Db 481 RIKARSLRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSAPKQAPPVRLNHQSGFS 540
QY 541 LSGSQADDDHIAARTAKIMAPPGGRSNTSL 571
Db 541 LSGAQIDDDNIPRRTTQRIVAPPGGRANITSL 571

RESULT 14
Q719G2 PRELIMINARY; PRT; 676 AA.
AC Q719G2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Collapsein response mediator protein-2A.
GN Name=CRMP2A;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22699123; PubMed=12814366;
RA Yuasa-Kawada J., Suzuki R., Kano F., Ohkawara T., Murata M., Noda M.;
RT "Axonal morphogenesis controlled by antagonistic roles of two CRMP
RL subtypes in microtubule organization.";
DR Eur. J. Neurosci. 17:2329-2343(2003).
DR EMBL; AF301549; AAK14487.1; -.
DR HSSP; P97427; 1KCX.

DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR011550; Amidohydro 1.
DR InterPro; IPR005847; DHOase.
DR Pfam; PF01979; Amidohydro 1; 1.
DR ProDom; PD001248; Amidohydro 1; 1.
DR ProDom; PD000518; DHOase; 1.
SQ SEQUENCE 676 AA; 73440 MW; 09F6404D0943856A CRC64;

Query Match      77.6%; Score 2315; DB 2; Length 676;
Best Local Similarity 75.0%; Pred. No. 6.9e-159;
Matches 429; Conservative 70; Mismatches 71; Indels 2; Gaps 1;

QY 2 SFQKKSIPIRIT--SDRLIRGRVNDQSFYADVHVDEGLIKQIGENLIVPGGIKTID 59
Db 104 SATGKEALQNLNDRLLIKGGKI VNDQSFYADYIMEDGLIKQIGENLIVPGGIKTIE 163
QY 60 AHGLMVLPGGVVHTRLOMPVLGMPADDFCGTGAALAGGTTMLDHDVFPDPTGVSLAA 119
Db 164 AGRMVLPGGIDVHTRFQMPQOGMTSADDFGTTGAALAGGTTMIIDHVVPDPTGVSLTA 223
QY 120 YEQWREADSAACDYSLSHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCSDS 179
Db 224 FQWREADSKSCDYSLSHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRFQLSDS 283
QY 180 QWYEPISIRDLGALAQAHAENGDI VEEBQKRLLELGTGPEGHVLSPHEVEAEAVYRA 239
Db 284 QIYEVLSVIRDIGAIAQAHAENGDI IAEAQORILDGLGTGPEGHVLSPHEVEAEAVNRA 343
QY 240 VTIKQANCLVYTKVMSKGAADAIQAQRGVVVFGEPI TASIGTDSHYMSKNAKAA 299
Db 344 ITIANQNCPLVYTKVMSKSAEAVIAQARKKGTVYGEPI TASIGTDSHYMSKNAKAA 403
QY 300 AFVTSPPVNPDPPTADHLTCLLSGGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIE 359
Db 404 AFVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIE 463
QY 360 RMSWWEKCVASGKNDENEFVATSTNAKIFNFPYPRKGRVAVGSDADLVINPKATKI 419
Db 464 RMSIIMDKAVVTGKMDENQFVATSTNAKIFNFPYPRKGRVAVGSDADLVINPKATKI 523
QY 420 ISAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVY 479
Db 524 ISAKTHNISLEYNIFEGMECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVY 583
QY 480 XRIKARNRLAEIHGVPRLGYPVHEVMVPAKPGSGAPARASCPGKISVPPVRLNHQSGF 539
Db 584 XRIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSAPKQAPPVRLNHQSGF 643
QY 540 LSGSQADDDHIAARTAKIMAPPGGRSNTSL 571
Db 644 LSGAQIDDDNIPRRTTQRIVAPPGGRANITSL 575

RESULT 15
Q6PB02 PRELIMINARY; PRT; 573 AA.
AC Q6PB02;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68668 protein.
GN Name=MGC68668;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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QY 481 RIKARNRLARIHGVPRGLYDGPVHVMPVPAKPGSGAPARASCPEGKISVPPVRLHQSGFS 540
 Db 481 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQAPVPRNLHQSGFS 540
 QY 541 LSGSQADDDHARRTAQKIMAPPGGRSNTSL 571
 Db 541 LSGAQIDDNIPTRTTORIVAPPGGRANITSL 571

RESULT 2
 S49985
 dihydropyrimidinase-related protein 2 [similarity] - rat
 N/Alternate names: collapsin response mediator protein 2; TOAD-64
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 13-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
 C/Accession: A59280, S49985
 R/Minturn, J.B.; Fryer, H.J.; Geschwind, D.H.; Hockfield, S.
 J. Neurosci. 15, 6757-6766, 1995
 A/Title: TOAD-64, a gene expressed early in neuronal differentiation in the rat, is related to the human TOAD-64 gene
 A/Reference number: A59280; MUID:56033765; PMID:7472434
 A/Accession: A59280
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-572 <MIN>
 A/Cross-references: UNIPROT:P47942; GB:246882; NID:G599965; PIDN:CAA86981.1; PID:G599968
 A/Experimental source: strain Sprague-Dawley; clone TOAD64 (turned on after division, 64)
 A/Note: submitted to the EMBL Data Library, November 1994
 A/Note: in Genbank entry R10AD64, release 113.0, the source is designated as Rattus rattus
 C/Superfamily: allantoinase; Bacillus dihydroorotase homology

Query Match 78.8%; Score 2349; DB 2; Length 572;
 Best Local Similarity 76.0%; Pred. No. 5.3e-163;
 Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGKKSIPRTSDRLIRGGIRVNDQSFYADVHVVDGLIKQIGENLIVPGIKTIDA 60
 Db 1 MSYQKKNIPIRTSDRLIRGGIRVNDQSFYADVHVVDGLIKQIGENLIVPGIKTIEA 60
 QY 61 HGLMVLPGVDVHTRQLMPVLGTPADDPCQGTAKALAGGTTMLDHPVDPDTCVSLAAY 120
 Db 61 HSRMVLPGGIDVHTRFQMPQDQMTSADDPFGGTAKALAGGTTMIDHVPDPGTSLAIF 120
 QY 121 EQWRERADSAACDYSILVDITRWHSISKEELALVKEGVNSFLVFMAYKRCQCSDSQ 180
 Db 121 DQWRWADSKSCDYSILVDITWKKIQEEMALVKDHGVNSFLVFMAYKRCQCSDSQ 180
 QY 181 MYEIFSIRDLGALAQVHAENGDIVDEEQKRLLELGTGPEGHVLSHPEEVEAEAVYRAV 240
 Db 181 IYEVLSVIRDIGALAQVHAENGDIIEBEQKRLLELGTGPEGHVLSRPERVEAEAVNRSI 240
 QY 241 TIAQANCPLYVTKWMSKGAADAIQAOKRGVVVFGEPITASIGTDSHWYSKNWAKAAA 300
 Db 241 TIANQTNCPLYVTKWMSKSAEAVIAQARKKGTVVYGEPIITASIGTDSHWYSKNWAKAAA 300
 QY 301 FVTSPPVNPDPPTADHLTCLLSSGLQVTSAGHCTFTTAOKAVGKONFALIPEGTNGIER 360
 Db 301 FVTSPPVNPDPPTDFLNSLLSCGLQVTSAGHCTFTTAOKAVGKONFALIPEGTNGTEE 360
 QY 361 RMSVMWKECVASGKMDENEFVAVTSTNAAKIIFNYPKRGVAVGSDADLVINPKATKII 420
 Db 361 RMSVIMDKAVVTKMDENQFVAVTSTNAAKVFNLYPRKGRISVGSDADLVIMDPDSVKTI 420
 QY 421 SAKTHNLNRYNIPFEGVECEGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTPDPFVYK 480
 Db 421 SAKTHNSALEYNIPFEGMECRGSLVVISQGRKIVLEDTLHVTBEGSGRYIPRKPDPFVYK 480
 QY 481 RIKARNRLARIHGVPRGLYDGPVHVMPVPAKPGSGAPARASCPEGKISVPPVRLHQSGFS 540
 Db 481 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQAPVPRNLHQSGFS 540
 QY 541 LSGSQADDDHARRTAQKIMAPPGGRSNTSL 571


```
Db      540 LSGTQVDEGV-RSASKRIIVAPPGGRSNTLSL 570

RESULT 6
JC5316
dhhydropyrimidinase related protein 1 - human
C/Species: Homo sapiens (man)
C/Date: 01-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
R/Accession: JC5316, S58090
R/Hamajima, N.; Matsuda, K.; Sakata, S.; Tamaki, N.; Sasaki, M.; Nonaka, M.
Gene 180, 157-163, 1996
A/Title: A novel gene family defined by human dihydropyrimidinase and three related proteins
A/Reference number: JC5315; MUID:97128821; PMID:8973361
A/Accession: JC5316
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-572 <HAM>
A/Cross-references: UNIPROT:Q14194; DDBJ:D78012; NID:g1330237; PIDN:BAAL1190.1; PID:g1330237
A/Experimental source: fetal brain
R/Goshima, Y.; Nakamura, F.; Strittmatter, P.; Strittmatter, S.M.
Nature 376, 509-514, 1995
A/Title: Collapsin-induced growth cone collapse mediated by an intracellular protein related to collapsin
A/Reference number: S5889; MUID:95364923; PMID:7637782
A/Accession: S58890
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 64-503, 'H', 505-572 <GOS>
A/Cross-references: EMBL:U17278; NID:g982148; PIDN:AAA93201.1; PID:g982149
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1994
C/Comment: This protein is involved in nervous system development.
C/Genetics:
A/Gene: GDB:CRMP1; DRP-1; DPYSL1
A/Cross-references: GDB:S585714
C/Superfamily: allantoinase; Bacillus dihydroorotase homology

Query Match      72.3%; Score 2157; DB 2; Length 572;
Best Local Similarity 69.2%; Pred. No. 5e-149;
Matches 395; Conservative 85; Mismatches 91; Indels 0; Gaps 0;

Qy      1 MSYQKKKIPRITSDRLIRGGRVNDQSFYADVHVEGLIKQIGENLIVPG---GIKTIDAHGLMVLPGGV 60
Db      1 MSYQKKKIPRITSDRLIRGGRVNDQSFYADVHVEGLIKQIGENLIVPGGV 60

Qy      61 HGLMVLPGGVVHTRLOMPLGTPADDFCOGTTKALAGTMTILDHVPDTCVSLAAY 120
Db      61 NGRMVLPGGVVHTRLOMPLGTPADDFCOGTTKALAGTMTILDHVPDTCVSLAAY 120

Qy      121 EWRREADSAACDYSLSHVDITRWHESIKEELEALVKEKGVNSFLVFMAYKORCQSDSQ 180
Db      121 EKWHEADYKSCDYSLSHVDITRWHESIKEELEALVKEKGVNSFLVFMAYKQVYQMSDSQ 180

Qy      181 MYTIFSIIRDLGALAOVHAENGDI VEEBOKRLLELGTGPBGHVLSPHREVEAEVYRAV 240
Db      181 LYEAFTFLKGLGAVILVHAENGDLIAEQKRIELMGITGPEGHALSRPELEAEVRAI 240

Qy      241 TIAQANCPYITVKWSKGAADIAQAKRGVVVFGEPTASLTGDSHYWSKNWAKAA 300
Db      241 TIAGRINCPYITVKWSKGAADIAQAKRGVVVFGEPTASLTGDSHYWSKNWAKAA 300

Qy      301 FVTSPPVNPDPPTADHLTCLLSGDIQVTSAGHCTFTTAQAVGKONFALIPGTNGIEE 360
Db      301 FVTSPPVNPDPPTADHLTCLLSGDIQVTSAGHCTFTTAQAVGKONFALIPGTNGIEE 360

Qy      361 RMSMWKEKCVASGMDENEFVATSTNAKIFNYPKRGVAVGSDADLVINPNKATKII 420
Db      361 RMTVMWMDKAVATGMDENEFVATSTNAKIFNLYPRKGRVAVGSDADLVINPNKATKII 420

Qy      421 SATHNLNVEYNIPFEGVECEGAPAVISQGRVALEDGKMPVTPGAGRFPVPRKTF 480
Db      421 TAKSHKSAVEYNIPFEGVECEGAPAVISQGRVALEDGKMPVTPGAGRFPVPRKTF 480

Qy      481 RIKARNRLABIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPRNLHQSGFS 540
Db      481 RIKARNRLABIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPRNLHQSGFS 540
```

```
Db      481 RVKIRNKVFLGQVSGRMVDPGVYEVPAATKYATPAPSAKSPSKHQPPPIRNLHQSNFS 540

Qy      541 LSGSQADDDHIAARTAAQKIMAPPGGRSNTLSL 571
Db      541 LSGAQIDDDNPRRTGHRIVAPPGGRSNTLSL 571

RESULT 7
JC5315
dhhydropyrimidinase (EC 3.5.2.2) - human
A/Alternate names: 5,6-dihydropyrimidinase amidohydrolase; Hydantoinase
C/Species: Homo sapiens (man)
C/Date: 01-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
R/Accession: JC5315
R/Hamajima, N.; Matsuda, K.; Sakata, S.; Tamaki, N.; Sasaki, M.; Nonaka, M.
Gene 180, 157-163, 1996
A/Title: A novel gene family defined by human dihydropyrimidinase and three related proteins
A/Reference number: JC5315; MUID:97128821; PMID:8973361
A/Accession: JC5315
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-519 <HAM>
A/Cross-references: UNIPROT:Q14117; DDBJ:D78011; NID:g2339965; PIDN:BAAL1189.1; PID:g1330237
A/Experimental source: liver
C/Comment: This enzyme is Zn2+-metalloenzyme, and the second enzyme involved in uracil aryl
dithymine to N-carbamyl-beta-aminoisobutyrate. It catalyzes the hydrolysis of a variety
of dithymine to N-carbamyl-beta-aminoisobutyrate.
C/Genetics:
A/Gene: GDB:DPYS; DHPase
A/Cross-references: GDB:S5885803
C/Complex: homotetramer
C/Superfamily: allantoinase; Bacillus dihydroorotase homology
C/Keywords: hydrolase

Query Match      52.2%; Score 1556; DB 2; Length 519;
Best Local Similarity 59.3%; Pred. No. 2.4e-105;
Matches 292; Conservative 70; Mismatches 126; Indels 4; Gaps 1;

Qy      16 RLLIGGRVNDQSFYADVHVEGLIKQIGENLIVPG---GIKTIDAHGLMVLPGGV 71
Db      6 RLLIGGRVNDQSFYADVHVEGLIKQIGENLIVPG---GIKTIDAHGLMVLPGGV 65

Qy      72 VHTRLQMPVLGTPADDFCOGTTKALAGTMTILDHVPDTCVSLAAYEOWREADSA 131
Db      72 VHTRLQMPVLGTPADDFCOGTTKALAGTMTILDHVPDTCVSLAAYEOWREADSA 125

Qy      132 CDYSLSHVDITRWHESIKEELEALVKEKGVNSFLVFMAYKORCQSDSQSYIFSIIRD 191
Db      132 CDYSLSHVAVTWMSDQVKEEMKILVQDKGVNSFLVFMAYKOLYMTDLELYEAFSRCKE 185

Qy      192 GALAOVHAENGDI VEEBOKRLLELGTGPBGHVLSPHREVEAEVYRAVTTIAQANCP 251
Db      186 GALAOVHAENGDLIAEQKRIELMGITGPEGHALSRPELEAEVRAITIASAVNCP 245

Qy      252 VTKWSKGAADIAQAKRGVVVFGEPTASLTGDSHYWSKNWAKAAAFVTSPPVNPDP 311
Db      246 IVTVWSKSAKVIADARRDKVYGEPTAASLTGDTHTYWNKEHHAHHVWGPP 305

Qy      312 TTADHLTCLLSGDIQVTSAGHCTFTTAQAVGKONFALIPGTNGIEERMSMWKEK 371
Db      306 STPDFLMLNLLANDLTTGTDCNTCTCOKALGKDDFTKIPNGVNGVEDRMSVWEK 365

Qy      372 SGMDENEFVATSTNAKIFNYPKRGVAVGSDADLVINPNKATKIIISAKTHNLN 431
Db      366 SGMDENEFVATSTNAKIFNLYPRKGRVAVGSDADLVINPNKATKIIISAKTH 425

Qy      432 NTFEGVECEGAPAVISQGRVALEDGKMPVTPGAGRFPVPRKTFPPDFVYKRI 491
Db      426 NTFEGVECEGAPAVISQGRVALEDGKMPVTPGAGRFPVPRKTFPPDFVYKRI 485

Qy      492 HGVPRGLYDGPV 503
Db      486 TPVERAPYKGEV 497
```


A/Accession: PC2206
A/Molecule type: protein
A/Residues: 1-20 <MU2>
C/Comment: This enzyme is a metalloenzyme and the oligomeric structure is required for a
C/Superfamily: allantoinase; Bacillus dihydroorotase homology
C/Keywords: hydrolase

Query Match 28.1%; Score 838; DB 1; Length 471;
Best Local Similarity 40.0%; Pred. No. 3.8e-53;
Matches 183; Conservative 80; Mismatches 191; Indels 4; Gaps 4;

QY	18	LIRGRIVNDQSFYADVDELIQIGENLIVPGGIKTIDAHGLMLVPGGVVDVHTRLQ	77
DB	4	LIRGRIVNDQSFYADVDELIQIGENLIVPGGIKTIDAHGLMLVPGGVVDVHTRLQ	77
QY	78	MPVLGMPADDDPCGGTKAALAGTTMLDHRVFPDGTGVSLLAAVEQWRERADSAACCDYSL	137
DB	63	MPFGGTVTKDDPESGTTAAAFGGTTIIDFCLTNKGEPLKKAETWHNKATGKAVIDYGF	122
QY	138	HVDITRWHSIKKELEALVKEGVNSPLVPMAYKDRQCSDSOMYEIPISTIRDLGALAQV	197
DB	123	HLMISITDDVLEELPKVIEEGITSFKVPFMAVKDFVQADDGTLXETLVAAKELGALVMV	182
QY	198	HAENGDIVSEEQKRLLELGTGPEGHVLSHPPEVEAEAVYRAVTIAKQANCPLYYTKVMS	257
DB	183	HAENGDIVSEEQKRLLELGTGPEGHVLSHPPEVEAEAVYRAVTIAKQANCPLYYTKVMS	257
QY	258	KGAADIAQAQRGVVVFGEPTASIGTDSHYMSKNMAKAAAFVTSPVNPDPPTTADHL	317
DB	243	AQAVEKIAEARNKGLNMGETCPQLVLDQSYLEKDNF-EGAKYVWSPPLR-EKMHQEV	300
QY	318	TCLSSGDLQVTSAGHCTFT-TAKAVGKDNFALIPGTINGIERMSMWKCVASGKMD	376
DB	301	WNAKNGQLQTLGSDQCSDFKQKELGRGDFTKIPNGGPIIEDRVSIILFSEGVKKGRIT	360
QY	377	ENEFVAVTSTNAKIFNFPYPRGRVAVGSDADLVWNPRAKTIISAKTNLNVENYIFEG	436
DB	361	LNQFVDIVSTRIAKLFGLPKKGTIAVGADADLVIFDPTVERVISAEETHMAVDYNPPEG	420
QY	437	VECRGAPAVVISQGRVALSDGKMFVTPGAGRFVPRKTF	474
DB	421	MKVTGEPVSVLCRGEFVVRDKQFVGKPGYQYVVKRKY	458

Search completed: September 24, 2005, 17:39:34
Job time : 274 secs

CC human immune deficiency viruses. CRMP is also used to identify agents
 CC potentially useful for treating prion diseases and to detect abnormal
 CC expression or localization of CRMP in immune system cells, for diagnosis
 CC and prognosis of diseases of the immune system. ABP97907-11 represent
 CC human CRMP proteins
 XX
 SQ Sequence 572 AA;

Query Match 99.9%; Score 2978; DB 6; Length 572;
 Best Local Similarity 99.8%; Pred. No. 5.4e-277;
 Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
 DB 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
 QY 61 HGLMWLPGGVDVHTRIQMPVLGWTADDFCQGTAAALAGTTMILDHVPDPTGVSLAAY 120
 DB 61 HGLMWLPGGVDVHTRIQMPVLGWTADDFCQGTAAALAGTTMILDHVPDPTGVSLAAY 120
 QY 121 EWRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCQSDSQ 180
 DB 121 EWRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCQSDSQ 180
 QY 181 MYEIPSIIRDGLAQAQVHAENGDIVEEOKRLELIGITGPEGHVLSPPEVEAEVYRAV 240
 DB 181 MYEIPSIIRDGLAQAQVHAENGDIVEEOKRLELIGITGPEGHVLSPPEVEAEVYRAV 240
 QY 241 TIAKQANCPLYVTKVMKGAADAIQAQKRGVVVFGEPIITASIGTDSHYWSKNWAKAA 300
 DB 241 TIAKQANCPLYVTKVMKGAADAIQAQKRGVVVFGEPIITASIGTDSHYWSKNWAKAA 300
 QY 301 FVTSPPVNPDPPTADHLTCLLSSGDLQVTSAGHCTPTTAQKAVGKONFALIPGTNGIBE 360
 DB 301 FVTSPPVNPDPPTADHLTCLLSSGDLQVTSAGHCTPTTAQKAVGKONFALIPGTNGIBE 360
 QY 361 RMSMWKVCVASKMDENEFVATSTNAKIFNYPKRGVAVGSDADLVINPKATKII 420
 DB 361 RMSMWKVCVASKMDENEFVATSTNAKIFNYPKRGVAVGSDADLVINPKATKII 420
 QY 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGVALEDKMFVTPGAGRFVPRKTFPDPVYK 480
 DB 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGVALEDKMFVTPGAGRFVPRKTFPDPVYK 480
 QY 481 RIKARNLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASC PGKISVPPVRNLHQSGFS 540
 DB 481 RIKARNLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASC PGKISVPPVRNLHQSGFS 540
 QY 541 LSGSQADDDHIARTAKINAPPGGRSNTLS 572
 DB 541 LSGSQADDDHIARTAKINAPPGGRSNTLS 572

RESULT 2

ID ADP65307
 XX ADP65307 standard; protein; 572 AA.
 AC ADP65307;
 XX
 XX 12-AUG-2004 (first entry)
 XX
 DE Human dihydropyrimidinase-like 4.
 XX
 XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 OS Homo sapiens.
 XX
 XX WO2003072827-A1.
 PN

XX 04-SEP-2003.
 PD
 XX 31-OCT-2002; 2002WO-US035433.
 PF
 XX 31-OCT-2001; 2001US-0336220P.
 PR
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA
 XX Hirsch R, Thornton SL;
 PI
 XX WPI: 2003-712740/67.
 DR
 XX GENBANK; NP_006417.
 DR
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 PT
 XX Disclosure; Page; 56pp; English.
 PS
 XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

Sequence 572 AA;

Query Match 99.9%; Score 2978; DB 7; Length 572;
 Best Local Similarity 99.8%; Pred. No. 5.4e-277;
 Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
 DB 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
 QY 61 HGLMWLPGGVDVHTRIQMPVLGWTADDFCQGTAAALAGTTMILDHVPDPTGVSLAAY 120
 DB 61 HGLMWLPGGVDVHTRIQMPVLGWTADDFCQGTAAALAGTTMILDHVPDPTGVSLAAY 120
 QY 121 EWRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCQSDSQ 180
 DB 121 EWRERADSAACDYSILHVDITRWHSIKKELEALVKEGVNSFLVFMAYKDRCCQSDSQ 180
 QY 181 MYEIPSIIRDGLAQAQVHAENGDIVEEOKRLELIGITGPEGHVLSPPEVEAEVYRAV 240
 DB 181 MYEIPSIIRDGLAQAQVHAENGDIVEEOKRLELIGITGPEGHVLSPPEVEAEVYRAV 240
 QY 241 TIAKQANCPLYVTKVMKGAADAIQAQKRGVVVFGEPIITASIGTDSHYWSKNWAKAA 300
 DB 241 TIAKQANCPLYVTKVMKGAADAIQAQKRGVVVFGEPIITASIGTDSHYWSKNWAKAA 300

QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIEE 360
DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIEE 360
QY 361 RSMWWEKCVASGKMDNEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
DB 361 RSMWWEKCVASGKMDNEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMPVTPGACRFVPRKTFPDPVYK 480
DB 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMPVTPGACRFVPRKTFPDPVYK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHVWVPAKPGSGAPARASCPGKISVPPVRLHQSGFS 540
DB 481 RIKARNRLAEIHGVPRGLYDGPVHVWVPAKPGSGAPARASCPGKISVPPVRLHQSGFS 540
QY 541 LSGSQADDDHARRTAQKINAPPGGRSNTLS 572
DB 541 LSGSQADDDHARRTAQKINAPPGGRSNTLS 572

RESULT 3
ADQ18668
ID ADQ18668 standard; protein; 572 AA.
AC ADQ18668;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 1487.
DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma;
XX
XX Example 2; SEQ ID NO 1487; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
XX Sequence 572 AA;

Query Match 99.9%; Score 2978; DB 8; Length 572;
Best Local Similarity 99.8%; Pred. No. 5.4e-277;
Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFQGGKSPRTSDRLIRGGRIVNDQSFYADVHVHVEDGLIKQIGENLIVPGIKTIDA 60
DB 1 MSFQGGKSPRTSDRLIRGGRIVNDQSFYADVHVHVEDGLIKQIGENLIVPGIKTIDA 60
QY 61 HGLMWLPGVVDVHTRQLQMPVLGWTTPADDFCOGTQKALAGGTTMLDHPVDFDTGVSLLAA 120
DB 61 HGLMWLPGVVDVHTRQLQMPVLGWTTPADDFCOGTQKALAGGTTMLDHPVDFDTGVSLLAA 120
QY 121 EQRERADSAACDYSLSHVDITRMHESIKEEALVKKGVSFLVFMAYKDCQCSDSQ 180
DB 121 EQRERADSAACDYSLSHVDITRMHESIKEEALVKKGVSFLVFMAYKDCQCSDSQ 180
QY 181 MYEIFSIIIRDLGALAQVHAENGDIVEEQRLLLELGTGPEGHVLSHPBEVEAEVYRAV 240
DB 181 MYEIFSIIIRDLGALAQVHAENGDIVEEQRLLLELGTGPEGHVLSHPBEVEAEVYRAV 240
QY 241 TIAKQANCPLYYTKVMSKGAADAIQAQRKRGVVVFGPEITASLGTDSHYWSKNWAKAAA 300
DB 241 TIAKQANCPLYYTKVMSKGAADAIQAQRKRGVVVFGPEITASLGTDSHYWSKNWAKAAA 300
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIEE 360
DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTINGIEE 360
QY 361 RSMWWEKCVASGKMDNEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
DB 361 RSMWWEKCVASGKMDNEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMPVTPGACRFVPRKTFPDPVYK 480
DB 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMPVTPGACRFVPRKTFPDPVYK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHVWVPAKPGSGAPARASCPGKISVPPVRLHQSGFS 540
DB 481 RIKARNRLAEIHGVPRGLYDGPVHVWVPAKPGSGAPARASCPGKISVPPVRLHQSGFS 540
QY 541 LSGSQADDDHARRTAQKINAPPGGRSNTLS 572
DB 541 LSGSQADDDHARRTAQKINAPPGGRSNTLS 572

RESULT 4
ABG32231
ID ABG32231 standard; protein; 572 AA.
XX
XX AC ABG32231;
XX
XX 05-NOV-2002 (first entry)
XX
XX Human Ulip4/CRMP3 protein.
XX
XX Human; Ulip4; CRMP3, collapsin response mediator protein;
XX Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;
XX paraneoplastic neurodegenerative disease; PND; myelination;
XX demyelination; remyelination; myelin disorder; multiple sclerosis;
XX autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;
XX human T lymphocyte virus 1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 56 /note= "Encoded by AAG"
FT Misc-difference 554.572 /note= "Not encoded by the DNA sequence appearing as
FT /note= "ABK91191"
XX
XX US2002119944-A1.


```

Db 1 MSFGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
QY 61 HGLMVLPGGVVDVHTRQLQMPVLGWTMPADDFCOGTKAALAGGTTMILDHVPDPTGVSLAAY 120
Db 61 HGLMVLPGGVVDVHTRQLQMPVLGWTMPADDFCOGTKAALAGGTTMILDHVPDPTGVSLAAY 120
QY 121 EQRERADSAACCDYSILHVDITRWHSIKEELALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
Db 121 EQRERADSAACCDYSILHVDITRWHSIKEELALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
QY 181 MYEIPSIIRDLGALAOVHAENGDIIVEEQRKLELIGITGPEGHVLSHPPEVEAEVYRAV 240
Db 181 MYEIPSIIRDLGALAOVHAENGDIIVEEQRKLELIGITGPEGHVLSHPPEVEAEVYRAV 240
QY 241 TIQAQNCPLVYTKWMSKGAADAIAQAKRGVVVFGPEPTASLGTDSHYWSKNWAKAAA 300
Db 241 TIQAQNCPLVYTKWMSKGAADAIAQAKRGVVVFGPEPTASLGTDSHYWSKNWAKAAA 300
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIEE 360
Db 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIEE 360
QY 361 RMSWWEKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
Db 361 RMSWWEKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGACRFVPRKTFPPDPVYK 480
Db 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGACRFVPRKTFPPDPVYK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHSGGFS 540
Db 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHSGGFS 540
QY 541 LSGSQADDDHIARR 553
Db 541 LSGSQADDDHIARR 553

RESULT 6
AAW68488 standard; protein; 572 AA.
XX
AC AAW68488;
XX
DT 08-DEC-1998 (first entry)
XX
DE Mouse ULIP-4 protein.
XX
KW Mouse; Unc-33-like phospho-protein; ULIP; rat; neoplasm; tumorigenesis;
KW neurodegenerative disorder; diagnosis.
XX
OS Mus musculus.
XX
PN FR2759701-A1.
XX
PD 21-AUG-1998.
XX
PF 19-FEB-1997; 97FR-00001961.
XX
PR 19-FEB-1997; 97FR-00001961.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Aguerre M, Belin MF, Honnorat J, Kolattukudy P, Quach TT, Byk T;
PI Sobel A;
XX
DR WPI; 1998-449610/39.
DR N-PSDB; AAV60817.
XX
PT Mouse and human ULIP poly:peptide(s) - useful in detection of para-
neoplastic neurological syndromes.

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XX Claim 1; Fig 11; 90pp; French.

XX This sequence represents the mouse Unc-33-like phospho-protein (ULIP)-4. The coding sequence was isolated based on similarity to the rat ULIP sequence. Proteins of the ULIP family or their corresponding nucleic acids can be used in compositions for treating neurodegenerative disorders and neoplasms, especially for para-neoplastic neurological syndromes and/or for the early diagnosis of tumorigenesis

XX Sequence 572 AA;

Query Match 94.2%; Score 2809; DB 2; Length 572;

Best Local Similarity 92.8%; Pred. No. 1e-260;

Matches 531; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

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QY 1 MSFGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
Db 1 MSFGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
QY 61 HGLMVLPGGVVDVHTRQLQMPVLGWTMPADDFCOGTKAALAGGTTMILDHVPDPTGVSLAAY 120
Db 61 HGLMVLPGGVVDVHTRQLQMPVLGWTMPADDFCOGTKAALAGGTTMILDHVPDPTGVSLAAY 120
QY 121 EQRERADSAACCDYSILHVDITRWHSIKEELALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
Db 121 EQRERADSAACCDYSILHVDITRWHSIKEELALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
QY 181 MYEIPSIIRDLGALAOVHAENGDIIVEEQRKLELIGITGPEGHVLSHPPEVEAEVYRAV 240
Db 181 MYEIPSIIRDLGALAOVHAENGDIIVEEQRKLELIGITGPEGHVLSHPPEVEAEVYRAV 240
QY 241 TIQAQNCPLVYTKWMSKGAADAIAQAKRGVVVFGPEPTASLGTDSHYWSKNWAKAAA 300
Db 241 TIQAQNCPLVYTKWMSKGAADAIAQAKRGVVVFGPEPTASLGTDSHYWSKNWAKAAA 300
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIEE 360
Db 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIEE 360
QY 361 RMSWWEKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
Db 361 RMSWWEKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII 420
QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGACRFVPRKTFPPDPVYK 480
Db 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGACRFVPRKTFPPDPVYK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHSGGFS 540
Db 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHSGGFS 540
QY 541 LSGSQADDDHIARRTAOKIMAPPGGRSNIITSL 572
Db 541 LSGSQADDDHIARRTAOKIMAPPGGRSNIITSL 572

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RESULT 7

AAE38226

ID AAE38226 standard; protein; 512 AA.

XX

AC AAE38226;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human enzyme (ENZYME) protein #18.

XX

KW Human; enzyme; ENZYME; immune disorder; infection; myocardial infarction; gene therapy; anaemia; acquired immune deficiency syndrome; infection; reproductive disorder; cardiovascular; eye; cell proliferation; cancer; AIDS; allergy; aschma; Addison's disease; diabetes; goitre; impotence; infertility; atherosclerosis; metabolic disorder.

XX

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OS Homo sapiens.
PN WO2003052075-A2.
XX
XX PD 26-JUN-2003.
XX
XX PP 12-DEC-2002; 2002WO-US040161.
XX
XX PR 14-DEC-2001; 2001US-0340357P.
XX PR 20-DEC-2001; 2001US-0342962P.
XX PR 21-DEC-2001; 2001US-0343558P.
XX PR 22-JAN-2002; 2002US-0351107P.
XX
XX PA (INCY-) INCYTE GENOMICS INC.
XX
XX PI Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe IJ, Khare R;
PI Tran UK, Kable AE, Richardson TW, Emerling BM, Lindquist EA;
PI Baughn MR, Hafalia AJA, Jin P, Swarnakar A, Li JX, Marquis JP;
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;
XX
XX DR WPI; 2003-533016/50.
XX DR N-PSDB; AAD57506.
XX
XX PT New human enzyme (ENZM) polypeptide, useful for preparing a composition
XX for treating a disease associated with decreased expression or
XX overexpression of ENZM e.g. cancer.
XX
XX PS Claim 1; Page 284-285; 264pp; English.
XX
XX CC The invention relates to human enzyme (ENZM) polypeptides and their
XX corresponding polynucleotides. ENZM sequences are useful for preparing a
XX composition for diagnosis or treating a disease or condition associated
XX with decreased expression or overexpression of functional ENZM. The
XX disorders include immune disorders (anaemia, allergy or asthma),
XX infectious disorders (viral, fungal, parasitic or protozoal infection),
XX immune deficiencies (acquired immune deficiency syndrome; AIDS),
XX metabolic disorder (Addison's disease, diabetes or goitre), reproductive
XX disorders (infertility or impotence), cardiovascular disorders
XX (atherosclerosis or myocardial infarction), eye disorders and cell
XX proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The
XX present sequence is human ENZM protein
XX
XX SQ Sequence 512 AA;

Query Match      88.1%; Score 2628; DB 6; Length 512;
Best Local Similarity 89.5%; Pred. No. 2.2e-243;
Matches 512; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 1 MSFQGGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSFQGGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
QY 61 HGLMVLPGGVVDVHTRIQMPVLGTMTPADDFCQGTAKAALAGTTMILDHVPDPTGVSLAAY 120
DB 61 HGLMVLPGGVVDVHTRIQMPVLGTMTPADDFCQGTAKAALAGTTMILDHVPDPTGVSLAAY 120
QY 121 EQWRREADNACDYSLSHVDITFWHSEIKBEELAKVKGVSFLVPMAYKDCQCSDSQ 180
DB 121 EQWRREADNACDYSLSHVDITFWHSEIKBEELAKVKGVSFLVPMAYKDCQCSDSQ 180
QY 181 MYEIFSIIRDLAGALQVHAENGDI VEEQKRLLELGTGPEGHVLSHPBEVEAEAYRAV 240
DB 181 MYEIFSIIRDLAGALQVHAENGDI VEEQKRLLELGTGPEGHVLSHPBEVEAEAYRAV 240
QY 241 TIAQANCPILYVTKVSKGAADIAQAKRGVVVFGPEPTASLGTGSGHYWSKNWAKAAA 300
DB 241 TIAQANCPILYVTKVSKGAADIAQAKRGVVVFGPEPTASLGTGSGHYWSKNWAKAAA 300
QY 301 FVTSPPVPDPTADHLTCLLSSGDIQVTSAGHCTFTTAQKAVGKDNFALIPGTNGIRE 360
DB 301 FVTSPPVPDPTADHLTCLLSSGDIQVTSAGHCTFTTAQKAVGKDNFALIPGTNGIRE 360
QY 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420

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DB 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
QY 421 SAKTNLNVENYINIFEGVECRGAPAVVISQGRVLEDGKMFVTPGAGRFPVPRKTFPDPFYVK 480
DB 421 SAKTNL-----427
QY 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRLNHQSGFS 540
DB 428 -----LAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRLNHQSGFS 480
QY 541 LSGSQADDDHIAARTAKIMAPGGRSNITSLS 572
DB 481 LSGSQADDDHIAARTAKIMAPGGRSNITSLS 512

RESULT 8
ADK70709
ID ADK70709 standard; protein; 574 AA.
XX
XX AC ADK70709;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Collapsin response mediator protein (CRMP) 3B SeqID.
XX
XX KW signal control molecule; collapsin response mediator protein; CRMP;
XX nerve growth cone; axial future edge; neural-network formation;
XX cell polarity; neurogenesis.
XX
XX OS Unidentified.
XX
XX PN JP2004000094-A.
XX
XX PD 08-JAN-2004.
XX
XX PF 31-MAY-2002; 2002JP-00160853.
XX
XX PR 31-MAY-2002; 2002JP-00160853.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX DR WPI; 2004-085208/09.
XX DR N-PSDB; ADK70708.
XX
XX PT Novel N-terminal variant polypeptide of signal control molecule collapsin
XX response mediator protein of nerve growth cone, useful for neural-network
XX formation.
XX
XX PS Disclosure; Fig 19; 94pp; Japanese.
XX
XX CC This invention relates to a novel variant of an intracellular signal
XX control molecule identified as the collapsin response mediator protein
XX (CRMP) that works within the steering mechanism of the nerve growth cone
XX in an axial future edge part. Specifically, it refers to an N-terminal
XX variant that exhibits a deletion, substitution or addition of an amino
XX acid in CRMP, as well as the appropriate monoclonal antibody. The present
XX invention describes the CRMP variant as useful for neural-network
XX formation and for the establishment of cell polarity during growth.
XX Furthermore, it can be efficiently used during the neurogenesis process.
XX This polypeptide sequence is a CRMP isoform of the invention.
XX
XX SQ Sequence 574 AA;

Query Match      84.5%; Score 2519; DB 8; Length 574;
Best Local Similarity 81.4%; Pred. No. 8.4e-233;
Matches 467; Conservative 57; Mismatches 48; Indels 2; Gaps 1;

QY 1 MSFQGGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSNPGKRSFGRTSQQILIKGGKIVNDQSFYADVHVEDGLIKQIGENLIVPGGVRTIDA 60
QY 61 HGLMVLPGGVVDVHTRIQMPVLGTMTPADDFCQGTAKAALAGTTMILDHVPDPTGVSLAAY 120

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Db 61 YGQLVFGGIDVHTRLQMAWKGASADDFYQGTAAALAGTTIMDHVLPAGTSLIAAY 120
QY 121 EQRERADSAACDYSLSHVDITWHSISKEELALVKEKGVNSFLVFMAYKDCQCSDSQ 180
Db 121 EQRQRADSRACDYLHIIDI PRWHESLREELALVKDGVNSFLVFMAYKDRLOCTDAQ 180
QY 181 MYEIFSIIRDLGALAAQVHAENGDIVVEEQRLLELGITGPEGHVLSHPPEVEAEAVYRAV 240
Db 181 MYEIFCIIRDLGALAAQVHAENGDIIEEQRLLDIGITGPEGHVLSRPEVEAEAVYRAI 240
QY 241 TIAKQANCPVYTKVMSKGAADAIQAQRKGVVVFGEPIITASIGTSGSHYWSKNWAKAA 300
Db 241 TIAKQANCPVYTKVMSKGAADVVAQAQRKGVVVFGEPIITASIGTSGSHYWSKNWAKAA 300
QY 301 FVTSPPVNPDPPTADHLTCLLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIBE 360
Db 301 FVTSPPSPDPPTPERLSLLSCGDLQVAGSAHCTFTTAQKAVGKONFALIPGTTNGIBE 360
QY 361 RMSMWKCVASGMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKII 420
Db 361 RMAIWEKCVSGKMDENDPVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKVI 420
QY 421 SAKTHNLNVEYNIPEGVECEGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYK 480
Db 421 SAKTHNLNVEYNIPEGTECHGAPAVVISQGVVLEDNLFVTEGSGRFVPRKTFPDPVYK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAK--PGSGAPARASCPGKISVPPVPRNLHOSG 538
Db 481 RIKARNRLAEIHGVPRGLYDGPVHDVVLSTKAVPTTAAASRIACAGKVPAPVPRNLHOSG 540
QY 539 FSLSGSQADHDHARRTAQKIMAPPGGRSNTISLS 572
Db 541 FSLSGSQADHDHARRTAQKIMAPPGGRSNTISLS 574

RESULT 9
ID ADK70696 standard; protein; 650 AA.
XX ADK70696;
AC ADK70696;
XX ADK70696;
DT 06-MAY-2004 (first entry)
XX Chicken CRMP3A protein isoform SeqID.
DE signal control molecule; collapsin response mediator protein; CRMP;
XX nerve growth cone; axial future edge; neural-network formation;
KW cell polarity; neurogenesis; chicken.
XX Gallus gallus.
XX OS
XX JP2004000094-A.
XX PN
XX PD
XX 31-MAY-2002; 2002JP-00160853.
XX PF
XX PR 31-MAY-2002; 2002JP-00160853.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2004-085208/09.
XX DR N-PSDB; ADK70695.
XX Novel N-terminal variant polypeptide of signal control molecule collapsin
PT response mediator protein of nerve growth cone, useful for neural-network
PT formation.
XX Claim 14; SEQ ID NO 6; 94pp; Japanese.
XX This invention relates to a novel variant of an intracellular signal
CC control molecule identified as the collapsin response mediator protein

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CC (CRMP) that works within the steering mechanism of the nerve growth cone
CC in an axial future edge part. Specifically, it refers to an N-terminal
CC variant that exhibits a deletion, substitution or addition of an amino
CC acid in CRMP, as well as the appropriate monoclonal antibody. The present
CC invention describes the CRMP variant as useful for neural-network
CC formation and for the establishment of cell polarity during growth.
CC Furthermore, it can be efficiently used during the neurogenesis process.
CC This polypeptide sequence is a chicken CRMP isoform of the invention.
XX Sequence 650 AA;
SQ

Query Match 83.4%; Score 2488; DB 8; Length 650;
Best Local Similarity 81.8%; Pred. No. 1e-229;
Matches 459; Conservative 56; Mismatches 44; Indels 2; Gaps 1;

QY 14 SDRLLIRGRIVNDQSFYADVHVREDGLIKOIGENLIVPGIKITIDAHGLMWLPGGVVDVH 73
Db 90 SQOLLIRGRIVNDQSFYADVHVREDGLIKOIGENLIVPGIKITIDAHGLMWLPGGVVDVH 149
QY 74 TRLQMPVLGMPADDFCQGTAAALAGTTIMDHVLPAGTSLIAAYEQWRQADSRACC 133
Db 150 TRLQMAVMGASADDFYQGTAAALAGTTIMDHVLPAGTSLIAAYEQWRQADSRACC 209
QY 134 DYSLSHVDITWHSISKEELALVKEKGVNSFLVFMAYKDCQCSDSQMTFPIIRDLGA 193
Db 210 DYALHIDI PRWHESLREELALVKDGVNSFLVFMAYKDRLOCTDAQMTFPIIRDLGA 269
QY 194 LAQVHAENGDIVVEEQRLLELGITGPEGHVLSHPPEVEAEAVYRAVTTAKQANCPVYT 253
Db 270 IAQVHAENGDIIEEQRLLDIGITGPEGHVLSRPEVEAEAVYRAITTAQANCPVYT 329
QY 254 KYMSKGAADAIQAQRKGVVVFGEPIITASIGTSGSHYWSKNWAKAAAFVTSPPVNPDPPT 313
Db 330 KYMSKGAADVVAQAQRKGVVVFGEPIITASIGTSGSHYWSKNWAKAAAFVTSPPVNPDPPT 389
QY 314 ADHLTCLLSSGDLQVTSAGHCTFTTAQKAVGKONFALIPGTTNGIBEERMSMWKCVASG 373
Db 390 PERLSLLSCGDLQVAGSAHCTFTTAQKAVGKONFALIPGTTNGIBEERMAIWEKCVSG 449
QY 374 KMDENEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKII SAKTHNLNVEYNI 433
Db 450 KMDENDFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKIVISAKTHNLNVEYNI 509
QY 434 FEGVECEGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYKRIKARNRLAEIHG 493
Db 510 FEGTECHGAPAVVISQGVVLEDNLFVTEGSGRFVPRKTFPDPVYKRIKARNRLAEIHG 569
QY 494 VPRGLYDGPVHEVMVPAK--PGSGAPARASCPGKISVPPVPRNLHOSGFSLSGQADHDHIA 551
Db 570 VPRGLYDGPVHDVVLSTKAVPTTAAASRIACAGKVPAPVPRNLHOSGFSLSGQADHDHVA 629
QY 552 RETAKKIMAPPGGRSNTISLS 572
Db 630 RRTAKKIMAPPGGRSNTISLS 650

RESULT 10
ADK70707
ID ADK70707 standard; protein; 572 AA.
XX ADK70707;
AC ADK70707;
XX ADK70707;
DT 06-MAY-2004 (first entry)
XX Collapsin response mediator protein (CRMP) 2B SeqID.
DE signal control molecule; collapsin response mediator protein; CRMP;
KW nerve growth cone; axial future edge; neural-network formation;
KW cell polarity; neurogenesis.
XX Unidentified.
XX OS
XX JP2004000094-A.
PN

```


Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSPQGGKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSYQGGKNIPIRITSDRLIRGGKI VNDQSFYADIVMEDGLIKQIGENLIVPGGVKTIEA 60

QY 61 HGLMVLPGGVVHTRIQMPVLGTMTPADDFCGTKAALAGGTTMILDHVPDPTGVSLAAY 120
DB 61 HSRMVLPGGIDVHTRIQMPDQGMTSADDFQGTKAALAGGTTMILDHVPEPGTSLAALF 120

QY 121 EQWREADSAACDYSLSHVDITRWHSIEKEELALVKEKGVNSFLVFMVKDRCCQSDSQ 180
DB 121 DQWREWADSKCCDYSLSHVDITEWHKGIQEBMALVKDHGVNSFLVFMVKDRFQLTDSQ 180

QY 181 MYBIFSIIRDLGALAOVHAENGDI VEEBQRLLELGTGPEGHVLSHPPEVEAEAVYRAV 240
DB 181 IYEVLSVIRDIGAIAOVHAENGDIABEQQRILDLGITGPEGHVLSRPEVEAEAVNRSI 240

QY 241 TIAKQANCPLYVTVMKSGAADAIAQAKRGVVVFGEPITASIGTDSHYWKNWAKAAA 300
DB 241 TIANQTNCPLYVTVMKSKSAARVIAQARKKGTVVYGEPIITASIGTDSHYWKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAOKAVGKDNFALIPEGTNGIEE 360
DB 301 FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAOKAVGKDNFTLIPGTNGTEE 360

QY 361 RMSMWKCVASGKMDENEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKII 420
DB 361 RMSVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRISVGSDADLVIMPDVSKTI 420

QY 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
DB 421 SAKTHNSALEYNIPEGMECRGSLVVISQGI VLEDGTLHVTEGSGRYIPRKEFPDPVYK 480

QY 481 RIKARNLAEIHGVPRLGDPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 540
DB 481 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTTPASSAKTSPAKQOAPPVRNLHOSGFS 540

QY 541 LSGSQADDDHIARRTAQKIMAPPGGRSNTSL 571
DB 541 LSGAQIDDDNIPRRTTORIVAPPGGRANITSL 571

RESULT 12

ADJ84279
ID ADJ84279 standard; protein; 572 AA.

XX AC ADJ84279;

XX DE 06-MAY-2004 (first entry)

XX DE Malayan black rat CRMP-2 (collapse response mediator protein 2) protein.

XX DE antimicrobial; antiinflammatory; cytostatic; infection; inflammation;

XX DE tumour formation; antisense therapy; Malayan black rat; CRMP-2;

XX DE collapse response mediator protein 2.

XX OS Rattus rattus.

XX PN WO2004003134-A2.

XX XX 08-JAN-2004.

XX XX 12-JUN-2003; 2003WO-US018481.

XX XX 26-JUN-2002; 2002US-0392020P.

XX XX (ISIS-) ISIS PHARM INC.

XX XX Monia BP, Freier SM, Manoharan M, Gaarde WA;

XX XX WPI; 2004-083026/08.

XX XX N-PSDB; ADJ84229.

XX

PT

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Query Match

Best Local Similarity

Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFQGGKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60

DB 1 MSYQGGKNIPIRITSDRLIRGGKI VNDQSFYADIVMEDGLIKQIGENLIVPGGVKTIEA 60

QY 61 HGLMVLPGGVVHTRIQMPVLGTMTPADDFCGTKAALAGGTTMILDHVPDPTGVSLAAY 120

DB 61 HSRMVLPGGIDVHTRIQMPDQGMTSADDFQGTKAALAGGTTMILDHVPEPGTSLAALF 120

QY 121 EQWREADSAACDYSLSHVDITRWHSIEKEELALVKEKGVNSFLVFMVKDRCCQSDSQ 180

DB 121 DQWREWADSKCCDYSLSHVDITEWHKGIQEBMALVKDHGVNSFLVFMVKDRFQLTDSQ 180

QY 181 MYBIFSIIRDLGALAOVHAENGDI VEEBQRLLELGTGPEGHVLSHPPEVEAEAVYRAV 240

DB 181 IYEVLSVIRDIGAIAOVHAENGDIABEQQRILDLGITGPEGHVLSRPEVEAEAVNRSI 240

QY 241 TIAKQANCPLYVTVMKSGAADAIAQAKRGVVVFGEPITASIGTDSHYWKNWAKAAA 300

DB 241 TIANQTNCPLYVTVMKSKSAARVIAQARKKGTVVYGEPIITASIGTDSHYWKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAOKAVGKDNFALIPEGTNGIEE 360

DB 301 FVTSPLSPDPPTDFLNSLLSCGDLQVTSAGHCTFTTAOKAVGKDNFTLIPGTNGTEE 360

QY 361 RMSMWKCVASGKMDENEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVIMNPKATKII 420

DB 361 RMSVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRISVGSDADLVIMPDVSKTI 420

QY 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480

DB 421 SAKTHNSALEYNIPEGMECRGSLVVISQGI VLEDGTLHVTEGSGRYIPRKEFPDPVYK 480

QY 481 RIKARNLAEIHGVPRLGDPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 540

DB 481 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTTPASSAKTSPAKQOAPPVRNLHOSGFS 540

QY 541 LSGSQADDDHIARRTAQKIMAPPGGRSNTSL 571

DB 541 LSGAQIDDDNIPRRTTORIVAPPGGRANITSL 571

RESULT 13

ABG32228

ID ABG32228 standard; protein; 572 AA.

XX AC ABG32228;

Decreasing levels of a preselected cellular mRNA in a cell, useful for treating or preventing a disease associated with a preselected cellular mRNA, comprises binding to the mRNA an antisense compound targeted to a splice site on the mRNA.

Disclosure; Page 161-163; 174pp; English.

The invention relates to a novel method for decreasing levels of a preselected cellular mRNA in a cell or tissue comprising binding to the preselected cellular mRNA an antisense compound which is specifically hybridizable with a splice site on the mRNA and which is not a substrate for RNase H when bound to the RNA. The method of the invention has antimicrobial, antiinflammatory and cytostatic applications and may be useful for decreasing levels of a preselected cellular mRNA in a cell or tissue and thus for treating or preventing a disease or condition associated with a preselected cellular mRNA or with a preselected target cellular protein, particularly infection, inflammation or tumour formation. The current sequence is that of the Malayan black rat CRMP-2 (collapse response mediator protein 2) protein of the invention.

Sequence 572 AA;

Query Match 78.8%; Score 2349; DB 8; Length 572;

Best Local Similarity 76.0%; Pred. No. 2e-216;

Matches 434; Conservative 70; Mismatches 67; Indels 0; Gaps 0;

```

XX 05-NOV-2002 (first entry)
XX Human Ulp2/CRMP2 protein.
XX Human; Ulp2; CRMP2; collapsin response mediator protein;
XX Unc-33-like protein; neurodegenerative disease; Alzheimer's disease;
XX paraneoplastic neurodegenerative disease; PND; myelination;
XX demyelination; remyelination; myelin disorder; multiple sclerosis;
XX autoimmune neurodegenerative disorder; HTLV-1 associated myelopathy;
XX human T lymphocyte virus 1.
XX Homo sapiens.
XX OS
XX PN US2002119944-A1.
XX
XX PD
XX
XX 29-AUG-2002.
XX
XX 09-NOV-2001; 2001US-00986632.
XX
XX 09-NOV-2000; 2000US-0246751P.
XX
XX (AGUE/) AGUERA M.
XX (BELI/) BELIN M.
XX (CHAR/) CHARRIER E.
XX (HONO/) HONORAT J.
XX (RICA/) RICARD D.
XX (ROGE/) ROGEMOND V.
XX
XX Aguera M, Belin M, Charrier E, Honorat J, Ricard D, Rogemond V;
XX WPI; 2002-627172/67.
XX N-PSDB; ABK91188.
XX
XX Prevention or treatment of myelin disorders, such as multiple sclerosis,
XX by administering an agent selected from a Ulp1/CRMP protein, a nucleic
XX acid coding for the protein, or an antibody directed against protein.
XX
XX Claim 12; Page 18-20; 44pp; English.
XX
XX The invention relates to a new method for prevention or treatment of
XX myelin disorders, comprises administering to a patient an effective
XX amount of an agent selected from a Ulp1 (Unc-33-like protein)/CRMP
XX (collapsin response mediator protein) protein, a nucleic acid coding for
XX Ulp1/CRMP, an antisense sequence capable of specifically hybridising with
XX the nucleic acid, an antibody directed against Ulp1/CRMP, or an aptamer
XX capable of binding Ulp1/CRMP, and a pharmacologically acceptable carrier.
XX Also included are methods of diagnosing a myelin disorder in a subject,
XX identifying agents useful for the prevention or treatment of myelin
XX disorders, using the Ulp1/CRMP proteins/nucleic acids, agents capable of
XX modulating the function or expression of the proteins (increasing or
XX decreasing), and a method for identifying an endogenous agent as a
XX therapeutic target for the prevention or the treatment of myelin
XX disorders. The agents are useful for preventing or treating a myelin
XX disorder such as multiple sclerosis or HTLV-1 (human T lymphocyte virus
XX 1) associated myelopathy and neurodegenerative diseases, Alzheimer's
XX disease, paraneoplastic neurodegenerative diseases (PND), autoimmune
XX neurodegenerative disorder. Ulp1/CRMP proteins are involved in
XX the processes of myelination, demyelination and remyelination. Antibodies
XX to a Ulp1/CRMP protein are useful for diagnosing a myelin disorder. The
XX present sequence represents Ulp2/CRMP2 protein
XX
XX Sequence 572 AA;
XX
XX Query Match 78.6%; Score 2345; DB 5; Length 572;
XX Best Local Similarity 75.7%; Pred. No. 4.8e-216;
XX Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;
XX
XX 1 MSFGKKSIPRITSDRLIRGGIRVNDQSFYADVHVHEDGLIKQIGENLVPGIKTIDA 60
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MSYQGNKIPRITSDRLIRGGIRVNDQSFYADYIMEDGLIKQIGENLVPGVGTIERA 60
XX
XX 61 HGLMWLPVGGVDVHTRLQMPVLGHTPADDFCQGTAKAALAGTTWILDHVPDTCVSLAAY 120

```

XX The specification describes the a method for the use of CRMP (collapsin
 CC response mediator protein) polynucleotides, polypeptides, antisense
 CC oligonucleotides and antibodies for treating diseases involving
 CC dysfunction of T lymphocytes. CRMP is overexpressed in T cells of
 CC patients with immune system disorders. Blocking of CRMP also blocks the
 CC effect of pathological prion proteins. CRMP are used for treating
 CC diseases involving dysfunction of T lymphocytes, i.e. T cell leukemia or
 CC lymphoma; viral infections; prion diseases and demyelinating
 CC neuroinflammatory diseases such as multiple sclerosis, specifically
 CC infection by herpes, measles, Epstein-Barr, human T-cell lymphotropic or
 CC human immune deficiency viruses. CRMP is also used to identify agents
 CC potentially useful for treating prion diseases and to detect abnormal
 CC expression or localization of CRMP in immune system cells, for diagnosis
 CC and prognosis of diseases of the immune system. ABP97907-11 represent
 CC human CRMP proteins
 XX
 SQ Sequence 572 AA;

Query Match 78.6%; Score 2345; DB 6; Length 572;
 Best Local Similarity 75.7%; Pred. No. 4.8e-216;
 Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 DB 1 MSYQGGKNIPIRITSDRLIRGGKIVNDQSFYADIYMEDGLIKQIGENLIVPGVKTIEA 60

QY 61 HGLMVLPGGVVDVHTRLOMPVLGTPADDFCQGTKAALAGGTTMILDHVPDPTGVSLLAAY 120
 DB 61 HSRWVPGGIDVHTRFQMPDQGTSAADFFQGTKAALAGGTTMILDHVPDPTGVSLLAAY 120

QY 121 EQRERADSAACDYSLSHVDITRWHSIYKEELEALVKHGVSFLVPMAYKDCQCSDSQ 180
 DB 121 DQWRWADSKSCDYSLSHVDISEWHKGIQSEMEALVKDHGVSFLVPMAYKDCQCSDSQ 180

QY 181 MYEIPSIIRDLGALAOVHAENGDIYVEEOKRLLLELIGITGPEGHVLSHPREVEAEAVRAV 240
 DB 181 IYEVLSVIRDIGAIAQVHAENGDIYAEQORILDIGITGPEGHVLSHPREVEAEAVRAV 240

QY 241 TIQAQNCPLVYITKVMKSGAADAIAQAKRGVVVFGPEPTASIGTDSHYWSKNWAKAAA 300
 DB 241 TIANQNTCNPLVYITKVMKSSAEVIAQAKRGVTVVYGEPTASIGTDSHYWSKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTTNGIEE 360
 DB 301 FVTSPLSPDPTTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTTNGTEE 360

QY 361 RMSWWEKCVASGKMDNEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
 DB 361 RMSVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRVAVGSDADLVINWPKATKII 420

QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 DB 421 SAKTHNSLSLEYNIFEGMECKSGPLVVISQKIVLEDTLHVTGSGRYIPRKFPDPVYK 480

QY 481 RIKARSLAEIRGVRGLYDGPVCEVSVTPKTVTTPASSAKTSAPAKQAPVVRNLHSGFS 540
 DB 481 RIKARSLAEIRGVRGLYDGPVCEVSVTPKTVTTPASSAKTSAPAKQAPVVRNLHSGFS 540

QY 541 LSGSQADHDHARTAKINAPPGRGNITSL 571
 DB 541 LSGAQIDDDNIPRRTTQRIVAPPGRGNITSL 571

RESULT 15
 ID ABM04810
 XX ABM04810
 AC ABM04810
 XX ABM04810
 DT 22-SEP-2003 (first entry)
 XX Human dihydropyrimidinase-related protein.

XX spinal cord; neuropathic pain; central sensitisation pain; pain;
 KW analgesic; gene therapy.
 XX Homo sapiens.
 XX EP1284298-A2.
 XX 19-FEB-2003.
 PD 26-JUL-2002; 2002EP-00255229.
 PP 27-JUL-2001; 2001GB-00018354.
 XX 07-FEB-2002; 2002GB-00002883.
 PR (WARN) WARNER LAMBERT CO.
 XX
 XX Brookebank RA, Dixon AK, Lee K, Pinnock RD;
 XX WPI; 2003-543489/52.
 DR N-PSDB; ACF25351.
 XX
 DR Use of an isolated gene sequence in the screening of compounds for
 PT diagnosing or treating pain.
 XX
 XX Claim 1; Page 97-99; 188pp; English.
 PS
 XX The invention relates to a novel isolated gene sequence that is
 CC downregulated in the spinal cord of a mammal in response to mechanically
 CC distinct first and second models of neuropathic or central sensitisation
 CC pain, useful in the screening of compounds for diagnosing or treating
 CC pain. A protein encoded by a gene of the invention has analgesic
 CC activity. A polynucleotide of the invention may have a use in gene
 CC therapy. The gene sequence is useful for preparing a composition for
 CC diagnosing or treating pain. The present sequence represents a protein
 CC encoded by a gene of the invention
 XX
 SQ Sequence 572 AA;

Query Match 78.6%; Score 2345; DB 6; Length 572;
 Best Local Similarity 75.7%; Pred. No. 4.8e-216;
 Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 DB 1 MSYQGGKNIPIRITSDRLIRGGKIVNDQSFYADIYMEDGLIKQIGENLIVPGVKTIEA 60

QY 61 HGLMVLPGGVVDVHTRLOMPVLGTPADDFCQGTKAALAGGTTMILDHVPDPTGVSLLAAY 120
 DB 61 HSRWVPGGIDVHTRFQMPDQGTSAADFFQGTKAALAGGTTMILDHVPDPTGVSLLAAY 120

QY 121 EQRERADSAACDYSLSHVDITRWHSIYKEELEALVKHGVSFLVPMAYKDCQCSDSQ 180
 DB 121 DQWRWADSKSCDYSLSHVDISEWHKGIQSEMEALVKDHGVSFLVPMAYKDCQCSDSQ 180

QY 181 MYEIPSIIRDLGALAOVHAENGDIYVEEOKRLLLELIGITGPEGHVLSHPREVEAEAVRAV 240
 DB 181 IYEVLSVIRDIGAIAQVHAENGDIYAEQORILDIGITGPEGHVLSHPREVEAEAVRAV 240

QY 241 TIQAQNCPLVYITKVMKSGAADAIAQAKRGVVVFGPEPTASIGTDSHYWSKNWAKAAA 300
 DB 241 TIANQNTCNPLVYITKVMKSSAEVIAQAKRGVTVVYGEPTASIGTDSHYWSKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTTNGIEE 360
 DB 301 FVTSPLSPDPTTDFLNSLLSCGDLQVTSAGHCTFTTAQKAVGKDNFALIPGTTNGTEE 360

QY 361 RMSWWEKCVASGKMDNEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
 DB 361 RMSVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRVAVGSDADLVINWPKATKII 420

QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 DB 421 SAKTHNSLSLEYNIFEGMECKSGPLVVISQKIVLEDTLHVTGSGRYIPRKFPDPVYK 480

Db	421	SANTHSSLEYNIFEGMECRGSPVVVISQKIVLEDTLHVTEGSGRYIPRKPPDFVYK	480
Qy	481	RIKARNRLAEIHCVPRGLYDGPVHEVMVPAPKPCSGAPABASCFCGLISVPPVRNLHQSGFS	540
Db	481	RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQQAAPPVRNLHQSGFS	540
Qy	541	LSGSQADDDHARRTAQKIMAPPGRSNITSL	571
Db	541	LSGAQIDDNI PRTTQRIVAPPGGRANITSL	571

Search completed: September 24, 2005, 17:11:29
Job time : 1138 secs

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OM protein - protein search, using sw model

Run on: September 24, 2005, 16:34:26 ; Search time 59 Seconds
(without alignments)
723.716 Million cell updates/sec

Title: US-09-367-496C-8
Perfect score: 2982
Sequence: 1 MSFQKKSIPRITSDRLIR.....RTAQKIMAPPGGRNITSLS 572

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2.6/prodata/1/iaa/5B COMB.pap.*
3: /cgn2.6/prodata/1/iaa/6A COMB.pap.*
4: /cgn2.6/prodata/1/iaa/6B COMB.pap.*
5: /cgn2.6/prodata/1/iaa/6C COMB.pap.*
6: /cgn2.6/prodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2345	78.6	572	4	US-09-949-016-6070
2	2345	78.6	578	4	US-09-949-016-11503
3	2152	73.5	570	4	US-09-949-016-6071
4	2152	73.5	593	4	US-09-949-016-10192
5	2157	72.3	572	4	US-09-702-705-1815
6	2157	72.3	572	4	US-09-736-457-1815
7	2157	72.3	572	4	US-09-671-325-1815
8	2157	72.3	622	4	US-09-949-016-10606
9	1074.5	36.0	470	4	US-09-949-016-11197
10	1074.5	36.0	507	4	US-09-252-991A-23541
11	1068	35.8	484	4	US-10-114-810-2
12	1041	34.9	495	4	US-09-734-237B-62
13	1041	34.9	496	4	US-09-734-237B-64
14	827	27.7	460	1	US-08-289-709-1
15	827	27.7	460	1	US-08-602-656-1
16	809	27.1	461	4	US-09-836-992-1
17	699.5	23.5	457	4	US-09-134-000C-6461
18	693.5	23.3	457	4	US-08-415-658-21
19	538.5	18.1	297	4	US-09-270-767-32995
20	538.5	18.1	297	4	US-09-270-767-48212
21	427	14.3	459	4	US-09-950-772-4
22	404.5	13.6	458	4	US-09-407-062-9
23	398.5	13.4	458	4	US-09-497-585A-8
24	398.5	13.4	458	4	US-09-497-585A-14
25	398.5	13.4	458	4	US-09-916-501A-14
26	398.5	13.4	458	4	US-09-916-501A-20
27	397.5	13.3	458	4	US-09-497-585A-4

28	397.5	13.3	458	4	US-09-916-501A-10	Sequence 10, Appl
29	396.5	13.3	458	4	US-09-497-585A-2	Sequence 2, Appl
30	396.5	13.3	458	4	US-09-497-585A-10	Sequence 10, Appl
31	396.5	13.3	458	4	US-09-497-585A-12	Sequence 12, Appl
32	396.5	13.3	458	4	US-09-916-501A-8	Sequence 8, Appl
33	396.5	13.3	458	4	US-09-916-501A-16	Sequence 16, Appl
34	396.5	13.3	458	4	US-09-916-501A-18	Sequence 18, Appl
35	392.5	13.2	458	4	US-09-497-585A-6	Sequence 6, Appl
36	392.5	13.2	458	4	US-09-916-501A-12	Sequence 12, Appl
37	311.5	10.4	454	4	US-09-134-000C-5977	Sequence 5977, Ap
38	262	8.8	411	4	US-09-270-767-33495	Sequence 33495, A
39	242.5	8.1	422	4	US-09-583-110-3844	Sequence 3844, Ap
40	242.5	8.1	426	4	US-09-107-433-3349	Sequence 3349, Ap
41	242	8.1	448	4	US-09-134-000C-6087	Sequence 6087, Ap
42	232	7.8	430	4	US-09-107-532A-5107	Sequence 5107, Ap
43	227	7.6	425	4	US-09-710-279-2604	Sequence 2604, Ap
44	227	7.6	427	3	US-09-134-001C-4803	Sequence 4803, Ap
45	212.5	7.1	734	4	US-09-902-540-11399	Sequence 11399, A

ALIGNMENTS

RESULT 1

US-09-949-016-6070
; Sequence 6070, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6070
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6070

Query Match	78.6%	Score	2345	DB	4	Length	572
Best Local Similarity	75.7%	Pred. No.	1.8e-237				
Matches	432	Conservative	72	Mismatches	67	Indels	0
Gaps	0						
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Db	1	MSYQKKNIPRITSDRLIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIEA	60				
Qy	61	HGLMVLPGGVVDVHTRQLQMEVLGTPADDFCQGTQKALAGTGMILHDPVDPDTCVSLAAY	120				
Db	61	HSEWIPGSDVHTRFQMPDQGTSDADFFQGTQKALAGTGMILHDPVDPDTCVSLAAY	120				
Qy	121	EQWRERASAAACDYSYLVHDIITRWHSIKKELEALVKEGVNSFLVFMAYKDCQCSDSQ	180				
Db	121	DQWRERASAAACDYSYLVHDIITRWHSIKKELEALVKEGVNSFLVFMAYKDCQCSDSQ	180				
Qy	181	MYEISFIRDLALQAQVHAENGDIIVEEQRLLLEIGITGPEGHVLSHPREVEAEAYRAV	240				
Db	181	MYEISFIRDLALQAQVHAENGDIIVEEQRLLLEIGITGPEGHVLSHPREVEAEAYRAV	240				
Qy	241	TIQAQNCPLVYTKWMSKGAADAIQAQRGVVVFGEPIITASLGTDGSHYWSKNWAKAAA	300				
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Db 301 FVTSPLSPDPTTDFLNSLLSCGDLQVTSAGHCTFNTAKAVGKDNFTLIPGTINGTEE 360
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Db 361 RSMVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRIAVGSDADLVWDPSVKTI 420
QY 421 SAKTNHLNVEYNIPEGVECRGAPVAVVISQGRVVALEDEGKMFVTPGAGRFPVPRKTFPDPFVK 480
Db 421 SAKTNHSSLEYNIPEGMECRGSPVAVVISQKIVLEDTGLHVTGSGRYIPRKPFPDPFVK 480
QY 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRLNHQSGFS 540
Db 481 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTTPASSAKTSPAKQQAAPPVRLNHQSGFS 540
QY 541 LSGSQADDDHARTTAQKIMAPPGRSNITSL 571
Db 541 LSGAQIDDDNIPRRTTORIVAPPGGRANITSL 571

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RESULT 2

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US-09-949-016-11503
; Sequence 11503, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11503
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11503

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Query Match 78.6%; Score 2345; DB 4; Length 578;
Best Local Similarity 75.7%; Pred. No. 1.9e-237;
Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGQKKSIPRITSRLLIRGGRIVNDQSFYADVHVHEDGLIKQIGENLIVPGGIKTIDA 60
Db 7 MSYQKKNIPRITSRLLIKGGKIVNDQSFYADIVMEDGLIKQIGENLIVPGVKTIEA 66
QY 61 HGLMVLPGGVVHTRLOMPVLGTPADDFCQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
Db 67 HERNVLPQGDIVHTRFQMPDQGMTSADDFQGTKAALAGTTMILDHVPDPTGVSLLAAY 126
QY 121 EOWREPADSAACDYSLSHYDITRWHSIKEELEALVKRKGVSFLVFMAYKORCQSDSQ 180
Db 127 DQWRWADSKSCDYSLSHYDISEMHKIQIBEMEALVKDHGVSFLVFMAYKORFQLTDCQ 186
QY 181 MYEIPSIIRDLGALQVHAENGDIIVEERQKRLLELQITGPEGHVLSHPPEVEAEAYRAV 240
Db 187 IYEVLSVIRDIGAIAQVHAENGDIIBEQOIRLDLQITGPEGHVLSRPEVEAEAVNRAI 246
QY 241 TTAKQANCPLYTKVMSKGAADIAQAKRGVVVFGEPTTASLGTGSHYMSKNWAKAAA 300
Db 247 TTANQNCPLXYTKVMSKSAEVIQAARKGTVVYGEPTTASLGTGSHYMSKNWAKAAA 306
QY 301 FVTSPPVNDPTTADHLTCLLSGDLQVTSAGHCTFNTAKAVGKDNFALIPGTINGIER 360
Db 307 FVTSPLSPDPTTDFLNSLLSCGDLQVTSAGHCTFNTAKAVGKDNFTLIPGTINGTEE 366

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QY 361 RSMVWEKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
Db 367 RSMVWDKAVVTGKMDENQFVAVTSTNAAKVFNLYPRKGRIAVGSDADLVWDPSVKTI 426
QY 421 SAKTNHLNVEYNIPEGVECRGAPVAVVISQGRVVALEDEGKMFVTPGAGRFPVPRKTFPDPFVK 480
Db 427 SAKTNHSSLEYNIPEGMECRGSPVAVVISQKIVLEDTGLHVTGSGRYIPRKPFPDPFVK 486
QY 481 RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRLNHQSGFS 540
Db 487 RIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTTPASSAKTSPAKQQAAPPVRLNHQSGFS 546
QY 541 LSGSQADDDHARTTAQKIMAPPGRSNITSL 571
Db 547 LSGAQIDDDNIPRRTTORIVAPPGGRANITSL 577

RESULT 3
US-09-949-016-6071
; Sequence 6071, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6071
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6071

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Query Match 73.5%; Score 2192; DB 4; Length 570;
Best Local Similarity 70.1%; Pred. No. 2.4e-221;
Matches 401; Conservative 91; Mismatches 78; Indels 2; Gaps 2;

QY 1 MSFGQKKSIPRITSRLLIRGGRIVNDQSFYADVHVHEDGLIKQIGENLIVPGGIKTIDA 60
Db 1 MSYQKKNIPRITSRLLIKGGKIVNDQSFYADIVMEDGLIKQIGENLIVPGVKTIEA 60
QY 61 HGLMVLPGGVVHTRLOMPVLGTPADDFCQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
Db 61 NGKMWIPQGDIVHTRFQMPYKGMTTVDFFQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
QY 121 EOWREPADSAACDYSLSHYDITRWHSIKEELEALVKRKGVSFLVFMAYKORCQSDSQ 180
Db 121 EKWREWADSKSCDYSLSHYDITRWNDSDVKQEVONLIDKRGVNSFMVYMAKOLYQVSNTE 180
QY 181 MYEIPSIIRDLGALQVHAENGDIIVEERQKRLLELQITGPEGHVLSHPPEVEAEAYRAV 240
Db 181 LYEIFTCLELGAIAQVHAENGDIIAEQOTRMLMGITGPEGHVLSRPELEAEAVFRAI 240
QY 241 TTAKQANCPLYTKVMSKGAADIAQAKRGVVVFGEPTTASLGTGSHYMSKNWAKAAA 300
Db 241 TTASQTCNCPLYTKVMSKSAADLIQARKKGNVVFGEPTTASLGTGSHYMSKNWAKAAA 300
QY 301 FVTSPPVNDPTTADHLTCLLSGDLQVTSAGHCTFNTAKAVGKDNFALIPGTINGIER 360
Db 301 FVTSPLSPDPTTDFLNSLLSCGDLQVTSAGHCTFNTAKAVGKDNFTLIPGTINGVIE 360
QY 361 RSMVWEKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVINWPKATKII 420
Db 361 RSMVWDKAVATGKMDENQFVAVTSTNAAKIFNLYPRKGRISVGSDSLVWDPDVAKIV 420

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QY 481 RIKARNRLAEIHGVRGLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 540
Db 481 RVKIRNKVFLQGVSRGMYDGPVIEVTPATPKYATPAPSAKSPKQHPPIRNLHOSNFS 540

QY 541 LSGSQADDAHIAARTAKIMAPPGRSNTSL 571
Db 541 LSGAQIDNNPRTGHRIVAPPGRSNTSL 571

RESULT 6
US-09-736-457-1815
; Sequence 1815, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1815
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1815
```

```
Query Match 72.3%; Score 2157; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 1.2e-217;
Matches 395; Conservative 85; Mismatches 91; Indels 0; Gaps 0;

QY 1 MSFGQKKSIPRITSRLLIRGGRIVNDQSFADVHVEDGLIKQIGENLIVPGIKTIDA 60
Db 1 MSYQKKSIPHITSRLLIRGGRIVNDQSLYADVLEGLIKQIGENLIVPGVKTIEA 60

QY 61 HGLMVLPGGVVHTRLQMPVLGTPADDFCQGTAAALAGGTTMILDHVPDVGSLAAY 120
Db 61 NGRMVIPIGGIDVNTYLQKPSQGMATAADDPFQGTAAALVGGTTMIIDHVVPEPGSSLLTSP 120

QY 121 EQRERADSAACDYSILHVDITRWHSIKEELEALVKEKGVNSPLVPMAYKDRCCQSDSQ 180
Db 121 EKWHEAADTKSCCDYSILHVDITSWYDGVREBEVLVQDKGVNSFQVYMAKYQMSDSQ 180

QY 181 MYEIFSIIIDLAGALAOVHAENGDI VEEQKRLLELIGITGPEGHVLSHPBEVBAEAVYRAV 240
Db 181 LYEAFTFLKGLGAVILVHAENGDLIAEQKRIILEMIGITGPEGHALSPELEAEAVFRAI 240

QY 241 TIAQANCPLYTVTKVMSKGAADIAQAKRGVVVFGPEPTASLGTGSHYWSKNWAKAAA 300
Db 241 TIAGRINCPVYITKVMKSAAADIIALARKKGPLVFGPEPTAASLGTGTHYWSKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLISGDLQVTSACHTPTTAQKAVGKONFALIPEGTNGIER 360
Db 301 FVTSPLSPDPPTPDYLTSLACGDLQVTSAGHCPYSTAQKAVGKONFTLIPGVNGIER 360

QY 361 RMSVMWEKCVASGKMDENEFAVTSNAAKIFNYPYRKGRAVAVGSDADLVINWPKATKII 420
Db 361 RMTVWDKAVATGKMDENQFVATVSTNAAKIFNLVYRKGRIAVGSDADVVINDPKLXTI 420

QY 421 SAKTHNLNVEYNIPFEGVECRGAPAVVISQGRVALEDKMFVTPGAGRFVPRKTFPPFVYK 480
Db 421 TAKSHKSAVEYNIFEGMECHGSPLVVISQGIKIVPEDGNINNVKGMGRFIPRKAPPEHLVY 480
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QY 481 RIKARNRLAEIHGVRGLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 540
Db 481 RVKIRNKVFLQGVSRGMYDGPVIEVTPATPKYATPAPSAKSPKQHPPIRNLHOSNFS 540

QY 541 LSGSQADDAHIAARTAKIMAPPGRSNTSL 571
Db 541 LSGAQIDNNPRTGHRIVAPPGRSNTSL 571
```

```
RESULT 7
US-09-671-325-1815
; Sequence 1815, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1815
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-1815
```

```
Query Match 72.3%; Score 2157; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 1.2e-217;
Matches 395; Conservative 85; Mismatches 91; Indels 0; Gaps 0;

QY 1 MSFGQKKSIPRITSRLLIRGGRIVNDQSFADVHVEDGLIKQIGENLIVPGIKTIDA 60
Db 1 MSYQKKSIPHITSRLLIRGGRIVNDQSLYADVLEGLIKQIGENLIVPGVKTIEA 60

QY 61 HGLMVLPGGVVHTRLQMPVLGTPADDFCQGTAAALAGGTTMILDHVPDVGSLAAY 120
Db 61 NGRMVIPIGGIDVNTYLQKPSQGMATAADDPFQGTAAALVGGTTMIIDHVVPEPGSSLLTSP 120

QY 121 EQRERADSAACDYSILHVDITRWHSIKEELEALVKEKGVNSPLVPMAYKDRCCQSDSQ 180
Db 121 EKWHEAADTKSCCDYSILHVDITSWYDGVREBEVLVQDKGVNSFQVYMAKYQMSDSQ 180

QY 181 MYEIFSIIIDLAGALAOVHAENGDI VEEQKRLLELIGITGPEGHVLSHPBEVBAEAVYRAV 240
Db 181 LYEAFTFLKGLGAVILVHAENGDLIAEQKRIILEMIGITGPEGHALSPELEAEAVFRAI 240

QY 241 TIAQANCPLYTVTKVMSKGAADIAQAKRGVVVFGPEPTASLGTGSHYWSKNWAKAAA 300
Db 241 TIAGRINCPVYITKVMKSAAADIIALARKKGPLVFGPEPTAASLGTGTHYWSKNWAKAAA 300

QY 301 FVTSPPVNPDPPTADHLTCLISGDLQVTSACHTPTTAQKAVGKONFALIPEGTNGIER 360
Db 301 FVTSPLSPDPPTPDYLTSLACGDLQVTSAGHCPYSTAQKAVGKONFTLIPGVNGIER 360

QY 361 RMSVMWEKCVASGKMDENEFAVTSNAAKIFNYPYRKGRAVAVGSDADLVINWPKATKII 420
Db 361 RMTVWDKAVATGKMDENQFVATVSTNAAKIFNLVYRKGRIAVGSDADVVINDPKLXTI 420

QY 421 SAKTHNLNVEYNIPFEGVECRGAPAVVISQGRVALEDKMFVTPGAGRFVPRKTFPPFVYK 480
Db 421 TAKSHKSAVEYNIFEGMECHGSPLVVISQGIKIVPEDGNINNVKGMGRFIPRKAPPEHLVY 480
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QY 481 RIKARNLAEIHGVRGLYDGPVHEWVPAKPSGAPARASCCKISVPPVRNLHSGGFS 540
Db 481 RVKIRNKVFLQVSRGMYDGPVYEPATPKYATPAPSAKSSPSKHOPPIRLHQS NFS 540
QY 541 LSGSQADDDHARRTAQKIMAPPGRSNTSL 571
Db 541 LSGAQIDDDNNPRRTGHRIVAPPGRSNTSL 571

RESULT 8
US-09-949-016-10606
; Sequence 10606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10606
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10606

Query Match 72.3%; Score 2157; DB 4; Length 622;
Best Local Similarity 69.2%; Pred. No. 1.3e-217; Indels 0; Gaps 0;
Matches 395; Conservative 85; Mismatches 91;

QY 1 MSFGKKSIPRITSDDLIGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
Db 51 MSFGKKSIPHITSDDLIGGRILINDQSLYADVLEGLIKQIGENLIVPGVKTIEA 110
QY 61 HGLWVLPGVDVHTRLOMPVLGMPADDFCGTKAALAGGTTMILDHVPDPTGVSLAA 120
Db 111 NGRMVPGGIDVNTYLOKPSQGTAAADDFQGTAAALVGGTTMILDHVPDPTGVSLT 170
QY 121 EOWREADSAAACDYSLSHVDITWHESIKELALVKEKGVNSFLVPMAYKDRCCSDSQ 180
Db 171 EKWEAATKSCCDYSLSHVDITSMYDGVREBELVLDQKGVNSFQVYMAKYQMSDSQ 230
QY 181 MYEIFSIRDLGALAOVHAENGDIIVEEQRLELGLITGPEGHVLSHPREVAEAVYRAV 240
Db 231 LYEAFTPLKGLGAVILVHAENGDLIAEQKRIELWGITGPEGHVLSHPREVAEAVYRAI 290
QY 241 TIAQANCPYLVTKVMSKGAADAIAQAKRGVGVVFGEPITASLGTDSGHYWSKNWAKAAA 300
Db 291 TIAGRINCPVYITKWSKSAADIALARKKGLVFGEPITASLGTDSGHYWSKNWAKAAA 350
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGCTTTAOKAVGKNPALLIPGTNGIE 360
Db 351 FVTSPLSPDPPTPDYLTSLACGDLQVTSAGCTTTAOKAVGKNPALLIPGTNGIE 410
QY 361 RMSMWKCVASGMDNBEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINWPKATKII 420
Db 411 RMTVWDKAVATGMDNBEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINWPKATKII 470
QY 421 SAKTHNLNVEYNIPEGVECRGAPVAVISQGRVALEDGKMFVTPCAGRFVPRKTFPPVYK 480
Db 471 TAKSHKSAVEYNIPEGVECRGAPVAVISQGRVALEDGKMFVTPCAGRFVPRKTFPPVYK 530
QY 481 RIKARNLAEIHGVRGLYDGPVHEWVPAKPSGAPARASCCKISVPPVRNLHSGGFS 540
Db 531 RVKIRNKVFLQVSRGMYDGPVYEPATPKYATPAPSAKSSPSKHOPPIRLHQS NFS 590

QY 541 LSGSQADDDHARRTAQKIMAPPGRSNTSL 571
Db 591 LSGAQIDDDNNPRRTGHRIVAPPGRSNTSL 621

RESULT 9

US-09-949-016-11197
; Sequence 11197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11197
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11197

Query Match 36.0%; Score 1074.5; DB 4; Length 470;
Best Local Similarity 51.1%; Pred. No. 8e-104;
Matches 211; Conservative 57; Mismatches 114; Indels 31; Gaps 4;

QY 73 HTRLOMPVLGMPADDFCGTKAALAGGTTMILDHVPDPTGVSLAAAYQWRRERASAC 132
Db 18 HTR-----TCSSPSWARGPSTTSTRAPSMIIDFAIPQKGGSLIEAFETWRSWADPKVC 70
QY 133 CDYSLHVDITWHESIKELALVKEKGVNSFLVPMAYKDRCCSDSQMVEIFSIIRDLG 192
Db 71 CDYSLHVAVWSDQVKEKGLVQKGVNSFQVYMAKYQMSDSQLELYEAFSRCKEIG 130
QY 193 ALAQVHAENGDIIVEEQRLELGLITGPEGHVLSHPREVAEAVYRAVTAQANCPYV 252
Db 131 ALAQVHAENGDLIAEGAKQMLALGITGPEGHVLSHPREVAEAVYRAVTAQANCPYV 190
QY 253 TKVMSKGAADAIAQAKRGVGVVFGEPITASLGTDSGHYWSKNWAKAAAFTVSPVNPDP 312
Db 191 VHVMSKSAKVADARRDKGVVYGEPIAASLGTGTHYWNKEWHAAHHVMPGLRDPDS 250
QY 313 TADHLTCLSSGDLQVTSAGCTTTAOKAVGKNPALLIPGTNGIEERMSVWKECVAS 372
Db 251 TPDFLNLNLANDDLTGTDNCTFNTCQKALGKDDFTKIPNGVNGVEDRMSVWKEGVHS 310
QY 373 GMDNBEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINWPKATKII-----SA 422
Db 311 GMDNBEFVAVTSTNAAKIFNYPKRGVAVGSDADLVINWPKATKII-----SA 370
QY 423 KTHNLNVEYNIPEGVECRGAPVAVISQGRVALEDGK-MFVTPCAGRFVPRKTF 474
Db 371 YKTNMNL-----PLQCLANARVHMEESMVIFVFSLSLTSLFICRTF 410

RESULT 10

US-09-252-991A-23541
; Sequence 23541, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136

		CURRENT APPLICATION NUMBER: US/09/252,991A			
		CURRENT FILING DATE: 1999-02-18			
		PRIOR APPLICATION NUMBER: US 60/074,788			
		PRIOR FILING DATE: 1998-02-18			
		PRIOR APPLICATION NUMBER: US 60/094,190			
		PRIOR FILING DATE: 1998-07-27			
		NUMBER OF SEQ ID NOS: 33142			
		SEQ ID NO 23541			
		LENGTH: 507			
		TYPE: PRT			
		ORGANISM: Pseudomonas aeruginosa			
		US-09-252-991A-23541			
		Query Match 36.0%; Score 1074.5; DB 4; Length 507;			
		Best Local Similarity 45.8%; Pred. No. 9.2e-104;			
		Matches 216; Conservative 81; Mismatches 166; Indels 9; Gaps 4;			
QY	17	LLIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDAHGLMVLPGGVVHTRL	76		
DB	31	LLIRGATVTHESYRADVLCAQLQIGENLETSPGCDVLDGGQYLMFGGIDPHTM	90		
QY	77	QMPVLGMPADDFCQGTKAALAGTTMLDHPDPTGVSLLAAYEOWRERADSAACDYS	136		
DB	91	QLPFMTGVASEDFPSGTAAGLAGGTTSIIDFVIEPNRQSLLEAFHTWRGWAQKSA-ADYG	149		
QY	137	LHVDITRWHEISKEELEALVKEGVNSFLVPMAYKDCQCSDSQMYEIPSIIRDLGALAQ	196		
DB	150	FHVAITWSEVAREMELVAQGVNSPKHFMAKNAIMADDTLVASPERCLQAGVPT	209		
QY	197	VHAENGDIIVEEQKRILLELIGITGPEGHVLSHPREVEAEAVYRAVTIAKQANCPLYYTKVM	256		
DB	210	VHAENGELVHLQKLLAQSLTGPEAHLSPRPQVEGEASRAIRTAETLGTPLYLHVS	269		
QY	257	SKGAADAIAQAKRGVVVFGPEPTASLGTGSHYWSKNWAKAAAFVTPSPVNPDPPTADH	316		
DB	270	SREALDEIAYARAKGPVYGEVLGHLDDLDSVYRHPDWATAAGYVMSPPFRP----	325		
QY	317	LTCL---LSGDLQVTSAGHCTTTAAQVGNFALIPGTNGIERMSMWKEKCVASG	373		
DB	326	QEALWRGLQSGNLHTTATDHCCFCAEQKMGRODFSKIPNGTAGIEDRMALLMDAGVNSG	385		
QY	374	KMDENFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKIISAKTHNLNVEYNI	433		
DB	386	RLSMHEFVALTSTNAKIFNLPRKGAIRVGADADLVMDPQGSRTLSAATHQVDFNI	445		
QY	434	FEVCGRGAAPVVISQGRVALEDGKMFVTPGAGRFVPRKTPFPDFVYKRIAR	485		
DB	446	FEGRTVRGIPSHSTISQKLLMAAGDLRAEPGAGRYVERPAYPS-VYEVLGRR	496		
RESULT 11					
		US-10-114-810-2			
		Sequence 2, Application US/10114810			
		Patent No. 6800465			
		GENERAL INFORMATION:			
		APPLICANT: Bristol-Myers Squibb Company			
		TITLE OF INVENTION: D-Hydantoinase From Ochrobactrum anthropi			
		FILE REFERENCE: ON0158-NP			
		CURRENT APPLICATION NUMBER: US/10/114,810			
		CURRENT FILING DATE: 2002-08-16			
		PRIOR APPLICATION NUMBER: US 60/281,150			
		PRIOR FILING DATE: 2001-04-03			
		NUMBER OF SEQ ID NOS: 10			
		SOFTWARE: Patent in version 3.1			
		SEQ ID NO 2			
		LENGTH: 484			
		TYPE: PRT			
		ORGANISM: Ochrobactrum anthropi			
		US-10-114-810-2			
		Query Match 35.8%; Score 1069; DB 4; Length 484;			
		Best Local Similarity 47.0%; Pred. No. 4.1e-103;			
		Matches 214; Conservative 80; Mismatches 155; Indels 6; Gaps 4;			
		CURRENT APPLICATION NUMBER: US/09/734,237B			
		Sequence 62, Application US/09734237B			
		Patent No. 6818752			
		GENERAL INFORMATION:			
		APPLICANT: Rozzell, J. David			
		APPLICANT: Bui, Peter			
		APPLICANT: Hua, Ling			
		TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION			
		FILE REFERENCE: B583:40608			
		CURRENT APPLICATION NUMBER: US/09/734,237B			
		CURRENT FILING DATE: 2000-12-08			
		PRIOR APPLICATION NUMBER: 09/494,921			
		PRIOR FILING DATE: 2000-01-31			
		NUMBER OF SEQ ID NOS: 79			
		SOFTWARE: Patent in version 3.1			
		SEQ ID NO 62			
		LENGTH: 495			
		TYPE: PRT			
		ORGANISM: Pseudomonas putida			
		US-09-734-237B-62			
		Query Match 34.9%; Score 1041; DB 4; Length 495;			
		Best Local Similarity 47.1%; Pred. No. 3e-100;			
		Matches 210; Conservative 72; Mismatches 156; Indels 8; Gaps 3;			
QY	17	LLIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDAHGLMVLPGGVVHTRL	76		
DB	3	LLIRGATVTHESYRADVLCAQLQIGENLETSGCDVLDGGQYLMFGGIDPHTM	62		
QY	77	QMPVLGMPADDFCQGTKAALAGTTMLDHPDPTGVSLLAAYEOWRERADSAACDYS	136		
DB	63	QLPFMTGVASEDFPSGTAAGLAGGTTSIIDFVIEPNQSLLEAFHTWRGWAQKSA-SDYG	121		
QY	137	LHVDITRWHEISKEELEALVKEGVNSFLVPMAYKDCQCSDSQMYEIPSIIRDLGALAQ	196		
DB	122	FHVAITWSEVAREMELVAQGVNSPKHFMAKNAIMADDTLVASPERCLQAGVPT	181		
QY	197	VHAENGDIIVEEQKRILLELIGITGPEGHVLSHPREVEAEAVYRAVTIAKQANCPLYYTKVM	256		

Db 182 VHAENGELVYHLQKLLAQMTGPEAHPRLSPQVEGEAASRAIRIAETIGTPLYVHHIS 241
Qy 257 SKGAADAIAQKRGVGVVFGPEPITASIGTDSHYWYKNAKAAAFVTSPPVNDPTTADH 316
Db 242 SREALDEITYARAKGPVYGEVLPGHLLDSDVTRDPDMATAAGYVMSPPFRP-----REH 297
Qy 317 LTCL---LSSGDLQVTSACHCTTTAAQKAVGKNFALIPGTTNGIERMSWWEKCVASG 373
Db 298 QEALWRGLQSGNLHTTATDHCFCBAEQKAMGRDDFSRIPNGTAGIEDRMVAVLWDAGVNSG 357
Qy 374 KMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVWPNKATKIISAKTHNLNVEYNI 433
Db 358 RLSMHFEVALTSTNTAKIFNLPKRGAIRVGADADLVMDPQGTRTLISAQTHHQRVDFNI 417
Qy 434 FEGVECRGAPAVVISQGRVALEDGKM 459
Db 418 FEGRTVGRVPSHTISQGRVWADGDL 443

RESULT 13
US-09-734-237B-64
; Sequence 64 Application US/09734237B
; Patent No. 6818752
; GENERAL INFORMATION:
; APPLICANT: Rozzell, J. David
; APPLICANT: Bui, Peter
; APPLICANT: Hua, Ling
; TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
; FILE REFERENCE: B583:40608
; CURRENT APPLICATION NUMBER: US/09/734,237B
; CURRENT FILING DATE: 2000-12-08
; PRIOR FILING DATE: 2000-12-08
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 64
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetic protein derived from Pseudomonas putida hydantoinase, h
; OTHER INFORMATION: aving a glycine residue inserted after the initiating methionine
US-09-734-237B-64

Query Match 34.9%; Score 1041; DB 4; Length 496;
Best Local Similarity 47.1%; Pred. No. 3e-100;
Matches 210; Conservative 72; Mismatches 156; Indels 8; Gaps 3;

Qy 17 LLIRGRVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDAHGLMVLPGGVVDVHTRL 76
Db 4 LLIRGATVVTBESSYPADVLCDGLIRAGINLEPPTDCEILDGSGQYLMPPGIDPHTHM 63
Qy 77 QMPVLGMPADDDFCQGTAKAALAGTTMILDHVPDPTGVSLAAVEQWRERADSAACDYS 136
Db 64 QLPFGMTVASDEDFPFGTAAGLAGGTTSIDFVFPNPOQLLEAFHTWRGWAQKSA-SDYG 122
Qy 137 LHVDITRWHSIKEELEALYKKGVSFLVPMAYKORCQSDSQMVEIPIIRDLGALAQ 196
Db 123 FVAITWSEQVAEEMGELVAKGVNSFKRFMAYKNAIMAAADDTLVASFRCICQLGAVPT 182
Qy 197 VHAENGDI VEEOKRLLELIGITGPEGHVLSHPREVEARAVYVAVTIAKOANCLPYTKVM 256
Db 183 VHAENGELVYHLQKLLAQMTGPEAHPRLSPQVEGEAASRAIRIAETIGTPLYVHHIS 242
Qy 257 SKGAADAIAQKRGVGVVFGPEPITASIGTDSHYWYKNAKAAAFVTSPPVNDPTTADH 316
Db 243 SREALDEITYARAKGPVYGEVLPGHLLDSDVTRDPDMATAAGYVMSPPFRP-----REH 298
Qy 317 LTCL---LSSGDLQVTSACHCTTTAAQKAVGKNFALIPGTTNGIERMSWWEKCVASG 373
Db 299 QEALWRGLQSGNLHTTATDHCFCBAEQKAMGRDDFSRIPNGTAGIEDRMVAVLWDAGVNSG 358

Qy 374 KMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVWPNKATKIISAKTHNLNVEYNI 433
Db 359 RLSMHFEVALTSTNTAKIFNLPKRGAIRVGADADLVMDPQGTRTLISAQTHHQRVDFNI 418
Qy 434 FEGVECRGAPAVVISQGRVALEDGKM 459
Db 419 FEGRTVGRVPSHTISQGRVWADGDL 444

RESULT 14
US-08-289-709-1
; Sequence 1, Application US/08289709
; Patent No. 5523224
; GENERAL INFORMATION:
; APPLICANT: Butscher, Helmut; Lang, Gunter; Popp, Friedrich
; TITLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the
; TITLE OF INVENTION: Production and Use
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,709
; FILING DATE: 12-AUGUST-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 43 28 829.4
; FILING DATE: 27-AUGUST-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5523224man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 460 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-289-709-1

Query Match 27.7%; Score 827; DB 1; Length 460;
Best Local Similarity 39.7%; Pred. No. 8.9e-78;
Matches 182; Conservative 79; Mismatches 193; Indels 4; Gaps 4;

Qy 18 LLIRGRVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDAHGLMVLPGGVVDVHTRLQ 77
Db 4 LLIRGATVVTBESSYPADVLCDGLIRAGINLEPPTDCEILDGSGQYLMPPGIDPHTHM 62
Qy 78 MPVLGMPADDDFCQGTAKAALAGTTMILDHVPDPTGVSLAAVEQWRERADSAACDYS 137
Db 63 MPFGGTVTKDDPESGTIAAFGGTTIIDFCLTNKGEPLKKALETWHNKAQKAVIDYGF 122
Qy 138 HVDITRWHSIKEELEALYKKGVSFLVPMAYKORCQSDSQMVEIPIIRDLGALAQV 197
Db 123 HLMISEITDDVLEELPKVIAEBGITSFKVFMAYKNVFPQADDGTLVYRTLVAAKELGALVMV 182
Qy 198 HAEENGDI VEEOKRLLELIGITGPEGHVLSHPREVEARAVYVAVTIAKOANCLPYTKVM 257
Db 183 HAEENGDI VYLLTKALAEAGNTBPIYHALTRPPEVEGEATGRACQLTELAGSGLYVHVTC 242
Qy 258 KGAADAIAQKRGVGVVFGPEPITASIGTDSHYWYKNAKAAAFVTSPPVNDPTTADHL 317

Db 243 AQAVERIAQARNKGLDVMGTCQYLVLDSQ-YLEKPDPEGAKYVWSPPLR-EKWHQEV L 300
QY 318 TCLSSGDLQVTSAGHCTFT-TAQAQVGNDFALIPETNGIIEERMSMWKCVASGKMD 376
Db 301 WNALKNGQLQTLGSDQCSDFPKQKELGRGDTKIPNGGPMVEDRVSLFSEGVKKGRIT 360
QY 377 ENFVAVTSTNAKIFNFPYPRKGRVAGSDADLVINPKATKIISAKTHNLNVEYNIFEG 436
Db 361 LNOFVDMSTRIAKLFGLPFRKGTIAVGSADLVIFDPIERVISAETHHMAVDYNAFEG 420
QY 437 VECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTF 474
Db 421 MKVTGEPVSVLCRGEFVVRDKQFVGKPGYQYLKAGCF 458

RESULT 15

US-08-602-656-1
Sequence 1, Application US/08602656
Patent No. 5679571
GENERAL INFORMATION:
APPLICANT: Burtcher, Helmut; Lang, Gunter; Popp, Friedrich
TITLE OF INVENTION: Recombinant D-Hydantoinase, A Process For the
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,656
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/289,709
FILING DATE: 12-AUGUST-1994
APPLICATION NUMBER: P 43 28 829.4
FILING DATE: 27-AUGUST-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5679571man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-602-656-1

Query Match 27.7%; Score 827; DB 1; Length 460;
Best Local Similarity 39.7%; Pred. No. 8.9e-78;
Matches 182; Conservative 79; Mismatches 193; Indels 4; Gaps 4;
QY 18 LIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDAGLMLVLPFGVDVHTRLQ 77
Db 4 IIKNGTIVATDTYEADLLIKDKGIAMIGQHL-EKGAVIDAKGCYVFPFGIDSHTHLD 62
QY 78 MPVLGWTTPADDFCGYKAAAGGTTMLDHFVDPDVGSLAAYEQWRERADSAACCDYSL 137
Db 63 MPFGGVTVKDDPESGTIAAFAFGGTTTIIDFCLTNKGEPLKKAISTWHNKAKGKAVIDYGF 122

QY 138 HVDITRWHSIKEELEALVKEKGVNSFLVFMAYKDRCCSDSQMSQYEIFSIIRDGLGALAQV 197
Db 123 HLMISITDDVLEELPKVIAEEGITSFKVFMAYKNVFCADDGTLRTLVAAKELGALVMV 182
QY 198 HAENGDIVEEBQKRLLELGITQPEGHVLSHPBEVEABAVYRAVTIAQANCPLYYTKVMS 257
Db 183 HAENGVDIDYLTKKALAEAGNTEPIYHALTRPPEVEGEATGRACQLTELAGSQLYVVHVTC 242
QY 258 KGAADAIQAQKRGVVVFGPEPITASLGTDGSHYWKWAKAAAFVTSPPVNPDPPTADHL 317
Db 243 AQAVERIAQARNKGLDVMGTCQYLVLDSQ-YLEKPDPEGAKYVWSPPLR-EKWHQEV L 300
QY 318 TCLSSGDLQVTSAGHCTFT-TAQAQVGNDFALIPETNGIIEERMSMWKCVASGKMD 376
Db 301 WNALKNGQLQTLGSDQCSDFPKQKELGRGDTKIPNGGPMVEDRVSLFSEGVKKGRIT 360
QY 377 ENFVAVTSTNAKIFNFPYPRKGRVAGSDADLVINPKATKIISAKTHNLNVEYNIFEG 436
Db 361 LNOFVDMSTRIAKLFGLPFRKGTIAVGSADLVIFDPIERVISAETHHMAVDYNAFEG 420
QY 437 VECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTF 474
Db 421 MKVTGEPVSVLCRGEFVVRDKQFVGKPGYQYLKAGCF 458

Search completed: September 24, 2005, 17:40:45
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2005, 17:34:57 ; Search time 113 Seconds
(without alignments)
2060.274 Million cell updates/sec

Title: US-09-367-496C-8

Perfect score: 2982
Sequence: 1 MSFQKKSIPRTSDRLLR.....RTAQKIMPPGGRSNTTSL 572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 segs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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 - 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2978	99.9	572	16	US-10-723-860-1487
2	2978	99.9	572	18	US-10-287-436A-1487
3	2978	99.9	572	18	US-10-287-436A-1248
4	2976	99.8	572	9	US-09-986-632-10
5	2917	97.8	559	16	US-10-618-281-74
6	2628	88.1	512	17	US-10-498-788-18
7	2345	78.6	572	9	US-09-986-632-4
8	2345	78.6	572	15	US-10-205-331-52
9	2345	78.6	572	16	US-10-788-792-128
10	2345	78.6	572	16	US-10-733-969A-95
11	2345	78.6	572	16	US-10-733-969A-100

12	2345	78.6	572	16	US-10-851-921-6	Sequence 6, Appli
13	2192	73.5	570	18	US-10-287-436A-485	Sequence 485, App
14	2192	73.5	570	18	US-10-287-436A-1181	Sequence 1181, Ap
15	2184	73.2	570	9	US-09-986-632-6	Sequence 6, Appli
16	2157	72.3	572	9	US-09-986-632-8	Sequence 8, Appli
17	2157	72.3	572	9	US-09-736-457-1815	Sequence 1815, Ap
18	2157	72.3	572	9	US-09-902-941-1815	Sequence 1815, Ap
19	2157	72.3	572	9	US-09-849-626-1815	Sequence 1815, Ap
20	2157	72.3	572	14	US-10-017-754-1815	Sequence 1815, Ap
21	2157	72.3	572	14	US-10-180-198-2	Sequence 2, Appli
22	2157	72.3	572	14	US-10-113-872-1815	Sequence 1815, Ap
23	2157	72.3	572	15	US-10-283-017-1815	Sequence 1815, Ap
24	2157	72.3	572	17	US-10-852-335A-110	Sequence 110, App
25	2101	70.5	573	16	US-10-618-281-70	Sequence 70, Appl
26	1934.5	64.9	532	16	US-10-408-765A-1676	Sequence 1676, Ap
27	1556	52.2	519	16	US-10-408-765A-410	Sequence 410, App
28	1469.5	49.3	564	9	US-09-986-632-2	Sequence 2, Appli
29	1469.5	49.3	564	14	US-10-220-042-2	Sequence 2, Appli
30	1469.5	49.3	564	18	US-10-220-335-204	Sequence 204, App
31	1443	48.4	579	16	US-10-618-281-78	Sequence 78, Appl
32	1208.5	40.5	638	18	US-10-450-763-50979	Sequence 50979, A
33	1071	35.9	539	16	US-10-437-963-118365	Sequence 118365,
34	1068	35.8	484	14	US-10-114-810-2	Sequence 2, Appli
35	1041	34.9	495	10	US-09-734-237B-62	Sequence 62, Appl
36	1041	34.9	495	18	US-10-989-488A-62	Sequence 62, Appl
37	1041	34.9	496	18	US-09-734-237B-64	Sequence 64, Appl
38	1041	34.9	496	18	US-10-989-488A-64	Sequence 64, Appl
39	905	30.3	268	18	US-10-504-582-156	Sequence 156, App
40	840	28.2	332	15	US-10-220-120-214	Sequence 214, App
41	826	27.7	485	15	US-10-424-599-244709	Sequence 244709,
42	819.5	27.5	332	16	US-10-363-829-337	Sequence 337, App
43	809	27.1	461	9	US-09-836-992-1	Sequence 1, Appli
44	725.5	24.3	438	14	US-10-176-584A-2	Sequence 2, Appli
45	714.5	24.0	462	14	US-10-190-471-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-723-860-1487
; Sequence 1487, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1487
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1487

Query Match	99.9%	Score	2978	DB	16	Length	572
Best Local Similarity	99.8%	Pred.	No. 2.4e-261				
Matches	571	Conservative	1	Mismatches	0	Indels	0
Gaps	0						
QY	1	MSFQKKSIPRTSDRLLRGRINVDQSFYADVHVDGLIKQIGENLIVPGIKTIDA	60				
Db	1	MSFQKKSIPRTSDRLLRGRINVDQSFYADVHVDGLIKQIGENLIVPGIKTIDA	60				
QY	61	HGLMVLPGGVVHTRIQMPVLGNTPADDFCQGTQKALAGATTMILHVPDPTGVSLAAY	120				
Db	61	HGLMVLPGGVVHTRIQMPVLGNTPADDFCQGTQKALAGATTMILHVPDPTGVSLAAY	120				

QY 121 EOWRERADSAACDYSLSHVDTITRWHSIKKEELALVKEGVNSFLVPMAYKDRCCQSDSQ 180
 DB 121 ERWRERADSAACDYSLSHVDTITRWHSIKKEELALVKEGVNSFLVPMAYKDRCCQSDSQ 180
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 DB 181 MYEIPFSIIRDLGALAQVHAENGDI VEEBQKRLLELGITGPEGHVLSHPBEVEAEAYRAV 240
 QY 241 TIAKQANCPLYTVTKWSKGAADAI AQAQRGVVVVFGPEPTASLGTGDSHYNSKNWAKAAA 300
 DB 241 TIAKQANCPLYTVTKWSKGAADAI AQAQRGVVVVFGPEPTASLGTGDSHYNSKNWAKAAA 300
 QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAAKAVGKDNFALIPGTTNGIEE 360
 DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAAKAVGKDNFALIPGTTNGIEE 360
 QY 361 RMSMWKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
 DB 361 RMSMWKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
 QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 DB 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 QY 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
 DB 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
 QY 541 LSGSQADDDHIARTAKIMAPPGGRSNTISLS 572
 DB 541 LSGSQADDDHIARTAKIMAPPGGRSNTISLS 572

RESULT 2

US-10-287-436A-399
 ; Sequence 399, Application US/10287436A
 ; Publication No. US20050202421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
 ; FILE REFERENCE: 10872.514696
 ; CURRENT APPLICATION NUMBER: US/10/287,436A
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: US 60/336,220
 ; PRIOR FILING DATE: 2001-10-31
 ; NUMBER OF SEQ ID NOS: 1446
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 399
 ; LENGTH: 572
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-287-436A-399

Query Match 99.9%; Score 2978; DB 18; Length 572;
 Best Local Similarity 99.8%; Pred. No. 2.4e-261;
 Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFQKKKSIPRITSDRLIRGGRI VNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 DB 1 MSFQKKKSIPRITSDRLIRGGRI VNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 QY 61 HGLMVLPGGVVHTRQLMPVLGMPVLTADDFCQGTKAALAGGTTMILDHVPDPTGVSLAAY 120
 DB 61 HGLMVLPGGVVHTRQLMPVLGMPVLTADDFCQGTKAALAGGTTMILDHVPDPTGVSLAAY 120
 QY 121 EOWRERADSAACDYSLSHVDTITRWHSIKKEELALVKEGVNSFLVPMAYKDRCCQSDSQ 180
 DB 121 ERWRERADSAACDYSLSHVDTITRWHSIKKEELALVKEGVNSFLVPMAYKDRCCQSDSQ 180
 QY 181 MYEIPFSIIRDLGALAQVHAENGDI VEEBQKRLLELGITGPEGHVLSHPBEVEAEAYRAV 240

DB 181 MYEIPFSIIRDLGALAQVHAENGDI VEEBQKRLLELGITGPEGHVLSHPBEVEAEAYRAV 240
 QY 241 TIAKQANCPLYTVTKWSKGAADAI AQAQRGVVVVFGPEPTASLGTGDSHYNSKNWAKAAA 300
 DB 241 TIAKQANCPLYTVTKWSKGAADAI AQAQRGVVVVFGPEPTASLGTGDSHYNSKNWAKAAA 300
 QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAAKAVGKDNFALIPGTTNGIEE 360
 DB 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAAKAVGKDNFALIPGTTNGIEE 360
 QY 361 RMSMWKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
 DB 361 RMSMWKCVASGKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
 QY 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 DB 421 SAKTHNLNVEYNIFEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFPVPRKTFPDPVYK 480
 QY 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
 DB 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
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 DB 541 LSGSQADDDHIARTAKIMAPPGGRSNTISLS 572

RESULT 3

US-10-287-436A-1248
 ; Sequence 1248, Application US/10287436A
 ; Publication No. US20050202421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
 ; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
 ; FILE REFERENCE: 10872.514696
 ; CURRENT APPLICATION NUMBER: US/10/287,436A
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: US 60/336,220
 ; PRIOR FILING DATE: 2001-10-31
 ; NUMBER OF SEQ ID NOS: 1446
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1248
 ; LENGTH: 572
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-287-436A-1248

Query Match 99.9%; Score 2978; DB 18; Length 572;
 Best Local Similarity 99.8%; Pred. No. 2.4e-261;
 Matches 571; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFQKKKSIPRITSDRLIRGGRI VNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 DB 1 MSFQKKKSIPRITSDRLIRGGRI VNDQSFYADVHVEDGLIKQIGENLIVPGIKTIDA 60
 QY 61 HGLMVLPGGVVHTRQLMPVLGMPVLTADDFCQGTKAALAGGTTMILDHVPDPTGVSLAAY 120
 DB 61 HGLMVLPGGVVHTRQLMPVLGMPVLTADDFCQGTKAALAGGTTMILDHVPDPTGVSLAAY 120
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 DB 241 TIAKQANCPLYTVTKWSKGAADAI AQAQRGVVVVFGPEPTASLGTGDSHYNSKNWAKAAA 300
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Db 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTTTAAQKAVGKONFALIPGNTGIEE 360
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Db 361 RMSMWKECVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
Qy 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYK 480
Db 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYK 480
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Db 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
Qy 541 LSGSQADHIIARRTAQKIMAPPGGRSNTISLS 572
Db 541 LSGSQADHIIARRTAQKIMAPPGGRSNTISLS 572

RESULT 4

US-09-986-632-10
; Sequence 10, Application US/09986632
; Patent No. US200201199441
; GENERAL INFORMATION:
; APPLICANT: AGUERA, Michelle
; TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention or
; FILE REFERENCE: P06974US01/BAS
; CURRENT APPLICATION NUMBER: US/09/986,632
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/246,751
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-632-10

Query Match 99.8%; Score 2976; DB 9; Length 572;
Best Local Similarity 99.8%; Pred. No. 3.7e-261;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSFGKKSIPIRTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
Db 1 MSFGKKSIPIRTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
Qy 61 HGLMVLPGGVVDVHTRLQMPVLGMPADDPCQGTAKAALAGGTTMILDHVPDGTGVSLLAAY 120
Db 61 HGLMVLPGGVVDVHTRLQMPVLGMPADDPCQGTAKAALAGGTTMILDHVPDGTGVSLLAAY 120
Qy 121 EQWRERADSAACDYSLSHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRQCSDSQ 180
Db 121 EQWRERADSAACDYSLSHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRQCSDSQ 180
Qy 181 MYEIFSITRDLGALAQVHAENGDIIVREEQKRLLELGTGPEGHVLSHPREVEAEVYRAV 240
Db 181 MYEIFSITRDLGALAQVHAENGDIIVREEQKRLLELGTGPEGHVLSHPREVEAEVYRAV 240
Qy 241 TIAQANCPLVYTKVMSKGAADALAQAKRRGVVVFGEPIITASLGTDGSHYWSKNWAKAAA 300
Db 241 TIAQANCPLVYTKVMSKGAADALAQAKRRGVVVFGEPIITASLGTDGSHYWSKNWAKAAA 300
Qy 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTTTAAQKAVGKONFALIPGNTGIEE 360
Db 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTTTAAQKAVGKONFALIPGNTGIEE 360
Qy 361 RMSMWKECVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420
Db 361 RMSMWKECVASGKMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKII 420

Qy 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYK 480
Db 421 SAKTHNLNVEYNIPEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYK 480
Qy 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
Db 481 RIKARNRLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPCGKISVPPVRNLHQS GFS 540
Qy 541 LSGSQADHIIARRTAQKIMAPPGGRSNTISLS 572
Db 541 LSGSQADHIIARRTAQKIMAPPGGRSNTISLS 572

RESULT 5

US-10-618-281-74
; Sequence 74, Application US/10618281
; Publication No. US20040219609A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony G.
; APPLICANT: Batell, David A.
; APPLICANT: Lyons, Eric H.
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: Methods for Modulating Proteases Not
; FILE REFERENCE: GC773-2
; CURRENT APPLICATION NUMBER: US/10/618,281
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/395,325
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-281-74

Query Match 97.8%; Score 2917; DB 16; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.2e-256;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SDRLLIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDAHLMLVLPGGVDVH 73
Db 1 SDRLLIRGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDAHLMLVLPGGVDVH 60
Qy 74 TRLQMPVLGMPADDPCQGTAKAALAGGTTMILDHVPDGTGVSLLAAYEQWRERADSAACC 133
Db 61 TRLQMPVLGMPADDPCQGTAKAALAGGTTMILDHVPDGTGVSLLAAYEQWRERADSAACC 120
Qy 134 DYSLSHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRQCSDSQMYEIFSITRDLGA 193
Db 121 DYSLSHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRQCSDSQMYEIFSITRDLGA 180
Qy 194 LAQVHAENGDIIVREEQKRLLELGTGPEGHVLSHPREVEAEVYRAVTTAKQANCPLVYT 253
Db 181 LAQVHAENGDIIVREEQKRLLELGTGPEGHVLSHPREVEAEVYRAVTTAKQANCPLVYT 240
Qy 254 KVMKGAADALAQAKRRGVVVFGEPIITASLGTDGSHYWSKNWAKAAAFTVSPVNPDPPT 313
Db 241 KVMKGAADALAQAKRRGVVVFGEPIITASLGTDGSHYWSKNWAKAAAFTVSPVNPDPPT 300
Qy 314 ADHLTCLSSGDLQVTSAGHCTTTAAQKAVGKONFALIPGNTGIEERMSVMWKECVASG 373
Db 301 ADHLTCLSSGDLQVTSAGHCTTTAAQKAVGKONFALIPGNTGIEERMSVMWKECVASG 360
Qy 374 KMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKIIISAKTHNLNVEYNI 433
Db 361 KMDNEFVAVTSTNAAKIFNFPYPRKGRVAVGSDADLVINWPKATKIIISAKTHNLNVEYNI 420
Qy 434 FEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYKRIKARNRLAEIHG 493
Db 421 FEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPPDFVYKRIKARNRLAEIHG 480

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QY 494 VPRGLDGPVHEVWPAKPGSGAPARASCPGKISVPPVRNLHOSGSLSGSQADDDIARR 553
|||||
Db 481 VPRGLDGPVHEVWPAKPGSGAPARASCPGKISVPPVRNLHOSGSLSGSQADDDIARR 540
|||||

QY 554 TAQIMAPPGGRSNTSLS 572
|||||
Db 541 TAQIMAPPGGRSNTSLS 559
|||||

RESULT 6
US-10-498-788-18
; Sequence 18, Application US/10498788
; Publication No. US20050118594A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Narinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Lee, Ernestine A.
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Khare, Reena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Erika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April J. A.
; APPLICANT: Jin, Pei
; APPLICANT: Swarnakar, Anita
; APPLICANT: Li, Joana X.
; APPLICANT: Marquis, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; APPLICANT: Elliott, Vicki S.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCES: PF-1312 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/343,558
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/351,107
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7506139CDI
US-10-498-788-18

Query Match 88.1%; Score 2628; DB 17; Length 512;
Best Local Similarity 89.5%; Pred. No. 1.4e-229;
Matches 512; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 1 MSFGKKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
|||||
Db 1 MSFGKKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
|||||

QY 61 HGLMVLPGGVVDVHTRLOMPVLGTMTPADDPCQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
|||||
Db 61 HGLMVLPGGVVDVHTRLOMPVLGTMTPADDPCQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
|||||

QY 121 EQRERADSAACDYSLVHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
|||||
```

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Db 121 EQRERADSAACDYSLVHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
|||||
QY 181 MYEIPSIIRDLAGALAQVHAENGDIYEEBQKRLLLELIGITGPEGHVLSHPBEVEAEAVYRAV 240
|||||
Db 181 MYEIPSIIRDLAGALAQVHAENGDIYEEBQKRLLLELIGITGPEGHVLSHPBEVEAEAVYRAV 240
|||||
QY 241 TIAQANCPLYYTKVMSKGAADAIQAOKRGVVVGEPIITASLGTGDSHYMSKNWAKAAA 300
|||||
Db 241 TIAQANCPLYYTKVMSKGAADAIQAOKRGVVVGEPIITASLGTGDSHYMSKNWAKAAA 300
|||||
QY 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKNFALIEPGETNGISE 360
|||||
Db 301 FVTSPPVNPDPPTADHLTCLSSGDLQVTSAGHCTFTTAQKAVGKNFALIEPGETNGISE 360
|||||
QY 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIINFYPRKGRVAVGSDADLVINPKATKII 420
|||||
Db 361 RMSMWKCVASGKMDNEFVAVTSTNAAKIINFYPRKGRVAVGSDADLVINPKATKII 420
|||||
QY 421 SAKTHNLVBYNIPEGVBCRGAPAVVISQGRVALLDGKMFVTPGAGRFPVPRKTFPPDVYK 480
|||||
Db 421 SAKTHNL----- 427
|||||
QY 481 RIKARNRLAEIHGVRGLYDGPVHEVWPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 540
|||||
Db 428 -----LAEIHGVRGLYDGPVHEVWPAKPGSGAPARASCPGKISVPPVRNLHOSGFS 480
|||||
QY 541 LSGSQADDDHARRTAQKIMAPPGGRSNTSLS 572
|||||
Db 481 LSGSQADDDHARRTAQKIMAPPGGRSNTSLS 512
|||||

RESULT 7
US-09-986-632-4
; Sequence 4, Application US/09986632
; Patent No. US20020119944A1
; GENERAL INFORMATION:
; APPLICANT: AGUERA, Michelle
; TITLE OF INVENTION: Modulation of Uilp/CRMP activity for the prevention or
; FILE OF INVENTION: treatment of myelin disorders
; FILE REFERENCE: P06974US01/BAS
; CURRENT APPLICATION NUMBER: US/09/986,632
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/246,751
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-986-632-4

Query Match 78.6%; Score 2345; DB 9; Length 572;
Best Local Similarity 75.7%; Pred. No. 8.7e-204;
Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;

QY 1 MSFGKKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
|||||
Db 1 MSFGKKSIPIRITSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
|||||

QY 61 HGLMVLPGGVVDVHTRLOMPVLGTMTPADDPCQGTKAALAGTTMILDHVPDPTGVSLLAAY 120
|||||
Db 61 HGRMVPVIGIDVHTRPMPDQGTMSADDPCQGTKAALAGTTMIDVHVPDPTGVSLLAAY 120
|||||

QY 121 EQRERADSAACDYSLVHVDITRWHSIKEELEALVKEKGVNSFLVPMAYKDRCCQSDSQ 180
|||||
Db 121 DQWRWADSKSCDYSLVHVDISEWHKIQIEEMALVKDHGVNSFLVPMAYKDRFQLTDCQ 180
|||||

QY 181 MYEIPSIIRDLAGALAQVHAENGDIYEEBQKRLLLELIGITGPEGHVLSHPBEVEAEAVYRAV 240
|||||
Db 181 IVEVLSVIRDIGAIAQVHAENGDIYEEBQKRLLLELIGITGPEGHVLSRBEVEAEAVNRAI 240
|||||
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QY 241 TIAQANCPLYITVKMSKGAADIAIAQARRGVVVGEPITASLGTDGSHYWSKNWAKAAA 300
DB 241 TIANOTNCPLYITVKMSKSAEIVIAQARRKGTVYGEPI TASLGTDGSHYWSKNWAKAAA 300
QY 301 FVTSPPVNDPTTADHLTCLLSGDLQVTSAGHCTTTAQAQVGNFALIPGTNGIEE 360
DB 301 FVTSPPVNDPTTDFLNSLLSCDQLQVTSAGHCTTNTAQAQVGNFALIPGTNGTTE 360
QY 361 RMSMWKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVWNPVKATKII 420
DB 361 RMSVWDKAVVTKMDENQFVAVTSTNAAKVFNLYPRKGRVAVGSDADLVWNPDSVKTI 420
QY 421 SAKTHNLNVEYNIFEGVECGAPAVVISQGRVALEDEGKMFVTPGAGRFVPRKTFPDPVYK 480
DB 421 SAKTHNSSEYNIFEGMECRGSLVVISQGIKIVLEDTLHVTEGSGRYIPRKFPDPVYK 480
QY 481 RIKARNLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHSGGFS 540
DB 481 RIKARSLAEIRGVPRGLYDGPVCEVSVPKTVTPASSAKTSPAKQAPPPVRNLHSGGFS 540
QY 541 LSGSQADDDHIARTTAQKIMAPPGGRSNTSL 571
DB 541 LSGAQIDDDNIPRRTQRIVAPPGGRANITSL 571

RESULT 8

US-10-205-331-52
; Sequence 52, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; PRIOR FILING DATE: 2002-07-24
; SOFTWARE: Patent In Ver. 2.1
; LENGTH: 572
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Dihydropyrimidine-related protein
US-10-205-331-52

Query Match 78.6%; Score 2345; DB 15; Length 572;
Best Local Similarity 75.7%; Pred. No. 8.7e-204;
Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;
QY 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSYQGGKNIPTSDRLIKGGKIVNDQSFYADIVMEDGLIKQIGENLIVPGVKTIEA 60
QY 61 HGLMVLPGVDVHTRLOMPVLGTMTPADDFQCGTKAALAGTMMILDHVPPDTCVSLAAY 120
DB 61 HSRMVI PGIDVHTRFQMPDQGMTSADDFQGTQKALAGTMMI IDHVVP EPGTSLAFA 120
QY 121 EOWREBADSACCDYSLHVDITRWHSIKEELEALVKEGVNSFLVPMAYKORCQSDSQ 180
DB 121 DQREWADSKSCDYSLHVDISEWHGKIQEEMALVKDHGVNSFLVPMAYKORFQITDCQ 180
QY 181 MYEIFSIRDLGALAQVHAENGDI VEEQKRLLELIGITGPEGHVLSHPBEVEAEVYRAV 240
DB 181 DQREWADSKSCDYSLHVDISEWHGKIQEEMALVKDHGVNSFLVPMAYKORFQITDCQ 180
QY 241 TIAQANCPLYITVKMSKGAADIAIAQARRGVVVGEPITASLGTDGSHYWSKNWAKAAA 300
DB 241 TIANOTNCPLYITVKMSKSAEIVIAQARRKGTVYGEPI TASLGTDGSHYWSKNWAKAAA 300

DB 241 TIANOTNCPLYITVKMSKSAEIVIAQARRKGTVYGEPI TASLGTDGSHYWSKNWAKAAA 300
QY 301 FVTSPPVNDPTTADHLTCLLSGDLQVTSAGHCTTTAQAQVGNFALIPGTNGIEE 360
DB 301 FVTSPPVNDPTTDFLNSLLSCDQLQVTSAGHCTTNTAQAQVGNFALIPGTNGTTE 360
QY 361 RMSMWKCVASGKMDENEFVAVTSTNAAKIFNFYPRKGRVAVGSDADLVWNPVKATKII 420
DB 361 RMSVWDKAVVTKMDENQFVAVTSTNAAKVFNLYPRKGRVAVGSDADLVWNPDSVKTI 420
QY 421 SAKTHNLNVEYNIFEGVECGAPAVVISQGRVALEDEGKMFVTPGAGRFVPRKTFPDPVYK 480
DB 421 SAKTHNSSEYNIFEGMECRGSLVVISQGIKIVLEDTLHVTEGSGRYIPRKFPDPVYK 480
QY 481 RIKARNLAEIHGVPRLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRNLHSGGFS 540
DB 481 RIKARSLAEIRGVPRGLYDGPVCEVSVPKTVTPASSAKTSPAKQAPPPVRNLHSGGFS 540
QY 541 LSGSQADDDHIARTTAQKIMAPPGGRSNTSL 571
DB 541 LSGAQIDDDNIPRRTQRIVAPPGGRANITSL 571

RESULT 9

US-10-788-792-128
; Sequence 128, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 128
; LENGTH: 572
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-788-792-128

Query Match 78.6%; Score 2345; DB 16; Length 572;
Best Local Similarity 75.7%; Pred. No. 8.7e-204;
Matches 432; Conservative 72; Mismatches 67; Indels 0; Gaps 0;
QY 1 MSFQGGKSIPTSDRLIRGGRIVNDQSFYADVHVEDGLIKQIGENLIVPGGIKTIDA 60
DB 1 MSYQGGKNIPTSDRLIKGGKIVNDQSFYADIVMEDGLIKQIGENLIVPGVKTIEA 60
QY 61 HGLMVLPGVDVHTRLOMPVLGTMTPADDFQCGTKAALAGTMMILDHVPPDTCVSLAAY 120
DB 61 HSRMVI PGIDVHTRFQMPDQGMTSADDFQGTQKALAGTMMI IDHVVP EPGTSLAFA 120
QY 121 EOWREBADSACCDYSLHVDITRWHSIKEELEALVKEGVNSFLVPMAYKORCQSDSQ 180
DB 121 DQREWADSKSCDYSLHVDISEWHGKIQEEMALVKDHGVNSFLVPMAYKORFQITDCQ 180
QY 181 MYEIFSIRDLGALAQVHAENGDI VEEQKRLLELIGITGPEGHVLSHPBEVEAEVYRAV 240
DB 181 DQREWADSKSCDYSLHVDISEWHGKIQEEMALVKDHGVNSFLVPMAYKORFQITDCQ 180
QY 241 TIAQANCPLYITVKMSKGAADIAIAQARRGVVVGEPITASLGTDGSHYWSKNWAKAAA 300
DB 241 TIANOTNCPLYITVKMSKSAEIVIAQARRKGTVYGEPI TASLGTDGSHYWSKNWAKAAA 300
QY 301 FVTSPPVNDPTTADHLTCLLSGDLQVTSAGHCTTTAQAQVGNFALIPGTNGIEE 360
DB 301 FVTSPPVNDPTTDFLNSLLSCDQLQVTSAGHCTTNTAQAQVGNFALIPGTNGTTE 360

RESULT 14

US-10-287-436A-1181
; Sequence 1181, Application US/10287436A
; Publication No. US2005020421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1181
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1181

Query Match 73.5%; Score 2192; DB 18; Length 570;
Best Local Similarity 70.1%; Pred. No. 7.1e-190;
Matches 401; Conservative 91; Mismatches 78; Indels 2; Gaps 2;

QY	1	MSFOGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKOIGENLIVPGGIKTIDA	60
DB	1	MSYQGGKNIPRITSDRLIRGGRIVNDQSFYADIYMEDGLIKQIGDNVIVPGVKTIEA	60
QY	61	HGLMWLPGGVDVHTRLQMPVLGTMTPADDFCQGTKAALAGGTTMILDHVPPDTCVSLAAY	120
DB	61	NGKMWIPGGIDVHTHFQMPYKGMTVDDFPQGTKAALAGGTTMIDHVVPESSITEAY	120
QY	121	EQWRERADSAACDYSLSHVDITRWHSIEKEELAEALVKEGVNSFLVFMAYKRCQSDSQ	180
DB	121	EKWREWADGKSCCDYALHVDITHWDSVKQEVQNLIKDKGVNSFMVYMAKOLYQVSNTE	180
QY	181	MYEIPSIIRDLGALAQVHAENGDIVEEOKRLELIGITGPEGHVLSHPREVEAEAYRAV	240
DB	181	LYEIFTCLEGALQVHAENGDIIAQOETRMLEMGITGPEGHVLSRPELEAEAVRAI	240
QY	241	TIQAQNCPLVYTKVMSKGAADAIQAQRGVVVFGEPTASIGTDGSHYWSKNWAKAAA	300
DB	241	TIASQTNCPVYTKVMSKSAADLISQARKKGNVVFGEPTASIGIDGTHYWSKNWAKAAA	300
QY	301	FVTSPPVPDPTADHLTCLLSSGDLQVTSAGHCTFTTAQAVGKONFALIPETNGIEE	360
DB	301	FVTSPLSPDPTPDYINSLLASGDLQLSGSAHCTFSTAQKAIKGNFTAIPEGTVGVEE	360
QY	361	RMSMWKCVASQKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII	420
DB	361	RMSVIWDKAVATGKMDENQFVATSTNAAKIFNLYPRKGRISVGSDDLVIWDPDAVKIV	420
QY	421	SAKTHNLNVEYNI FEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYK	480
DB	421	SAKNHQAAYNI FEGMELRGAPLVVICQKIMLEDGNLHVTCAGRFIPCSFSDYVYK	480
QY	481	RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRLHQSGFS	540
DB	481	RIKARKKADLHAPRGMYDGPVFDLTTPPKGTPAGSARGSPTRPN-PPVRLHQSGFS	539
QY	541	LSGSQADDDHARTAKINAPPGGRSNTLS	572
DB	540	LSGTQVDEGV-RSASKRIVAPPGGRSNTLS	570

RESULT 15

US-09-986-632-6
; Sequence 6, Application US/09986632
; Patent No. US2002011994A1
; GENERAL INFORMATION:
; APPLICANT: AGUERA, Michelle

; TITLE OF INVENTION: Modulation of Ulip/CRMP activity for the prevention or
; TITLE OF INVENTION: treatment of myelin disorders
; FILE REFERENCE: P06974US01/BAS
; CURRENT APPLICATION NUMBER: US/09/986,632
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/246,751
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-632-6

Query Match 73.2%; Score 2184; DB 9; Length 570;
Best Local Similarity 69.8%; Pred. No. 3.8e-189;
Matches 399; Conservative 92; Mismatches 79; Indels 2; Gaps 2;

QY	1	MSFOGKKSIPRITSDRLIRGGRIVNDQSFYADVHVEDGLIKOIGENLIVPGGIKTIDA	60
DB	1	MSYQGGKNIPRITSDRLIRGGRIVNDQSFYADIYMEDGLIKQIGDNVIVPGVKTIEA	60
QY	61	HGLMWLPGGVDVHTRLQMPVLGTMTPADDFCQGTKAALAGGTTMILDHVPPDTCVSLAAY	120
DB	61	NGKMWIPGGIDVHTHFQMPYKGMTVDDFPQGTKAALAGGTTMIDHVVPESSITEAY	120
QY	121	EQWRERADSAACDYSLSHVDITRWHSIEKEELAEALVKEGVNSFLVFMAYKRCQSDSQ	180
DB	121	EKWREWADGKSCCDYALHVDITHWDSVKQEVQNLIKDKGVNSFMVYMAKOLYQVSNTE	180
QY	181	MYEIPSIIRDLGALAQVHAENGDIVEEOKRLELIGITGPEGHVLSHPREVEAEAYRAV	240
DB	181	LYEIFTCLEGALQVHAENGDIIAQOETRMLEMGITGPEGHVLSRPELEAEAVRAI	240
QY	241	TIQAQNCPLVYTKVMSKGAADAIQAQRGVVVFGEPTASIGTDGSHYWSKNWAKAAA	300
DB	241	TIASQTNCPVYTKVMSKSAADLISQARKKGNVVFGEPTASIGIDGTHYWSKNWAKAAA	300
QY	301	FVTSPPVPDPTADHLTCLLSSGDLQVTSAGHCTFTTAQAVGKONFALIPETNGIEE	360
DB	301	FVTSPLSPDPTPDYINSLLASGDLQLSGSAHCTFSTAQKAIKGNFTAIPEGTVGVEE	360
QY	361	RMSMWKCVASQKMDENEFVATSTNAAKIFNFPYPRKGRVAVGSDADLVINPKATKII	420
DB	361	RMSVIWDKAVATGKMDENQFVATSTNAAKIFNLYPRKGRISVGSDDLVIWDPDAVKIV	420
QY	421	SAKTHNLNVEYNI FEGVECRGAPAVVISQGRVALEDGKMFVTPGAGRFVPRKTFPDPVYK	480
DB	421	SAKNHQAAYNI FEGMELRGAPLVVICQKIMLEDGNLHVTCAGRFIPCSFSDYVYK	480
QY	481	RIKARNRLAEIHGVPRGLYDGPVHEVMVPAKPGSGAPARASCPGKISVPPVRLHQSGFS	540
DB	481	RIKARKKADLHAPRGMYDGPVFDLTTPPKGTPAGSARGSPTRPN-PPVRLHQSGFS	539
QY	541	LSGSQADDDHARTAKINAPPGGRSNTLS	572
DB	540	LSGTQVDEGV-RSASKRIVAPPGGRSNTLS	570

Search completed: September 24, 2005, 17:50:06
Job time : 115 secs